

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
 CCTGGTGCACCACAC**CATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTACCAAGGCCTCCCTGTTGTGAAGAATTCATCAGCAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA
 GAAC**TG**GCCAAGA**ACT**CAAAAGAGGCAGCATTGGAACCATCGATGGAAAAATATTTAA**AA**TT
 GATCAGATGGGAAGATGGTTTGTCTGGAGGGGCTGCTGTTGGTCTTGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAA**TT**TGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAA**C**AGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAAC**TT**TCATGATGAGAGGCTCTTG
 GGTGACAATTTGGTGTGACCTTTCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCGGCCCAAAGCATCTTGCTTGGTTGCTACATTCGTGGTGTATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCA**GTG**AAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGCTCTTTGTGTCTCATTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGAT
 AGTCTTTTTCAGCATGTTCTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAATATGATCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCCAACAGAA**AAATG**
AAGTGACTCAGCTTCTGGCTTCTCTGTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGCTCGCCTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAAATAAGCACACACATTTCAATTCATGTTTGAAGTATTTTAAATGTT
 TTGGTGAATGTGA**AA**ACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTCTACTTTAA**AA**
 TTTAGTAGGTTCACTGAGTAAC**TAA**AATTTAGCAAACCTGTGTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACCAAGTGGTCATTGTTACATTCATT
 GCTGAAC**TTA**CAAA**AA**CTGTTTCATCTGAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCA**GT**TTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTACAAAGGAA
 ATAAC**TTT**AA**AA**CTATCTCAAGAGAAATATCAAGCATGAATATGTGCTTTTCCAG
 AATACAAACAGTATACTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWVFVAGGAAVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTLILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVLFMSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGCTCGGCCGCTTCCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGGGCGCGTCGTGAGGG
 GGTCCGACCGGGAGTCGCGCGGCTTGTGCATCTTGGCTACCTGTGGGTCGAAG**ATG**TCCGG
 ACATCGGAGACTGGTTCAGGAGCATCCCGGCATCACGCGCTATTGGTTCGCGCGCACCGTC
 CGCGTGCCTTGGTCCGCAAACTCGGCCCTCATCAGCCCGGCCTACCTCTTCTCTCGGCCGA
 AGCCTCTCTTTATTCGTTTTCAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG
 GTCCAGGAAGCTGGATTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA
 CTTGAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
 TGTCAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGGG
 ACACGATTTAAGGCCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATGGAAATCTGGTTGGACATCTTTATTTTTCCTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTGTGATCCGCTGG
 CTGCCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGGAGGCGGGAGACAACTGGGGCCAGGGCTTTCGACTTGGAGACC
 AG**TCGA**AGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCCCTCCAGTGCTGGGTG
 CACTTAAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTTC
 AGTCAGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAAGTTTTCAGCAT
 TCTCATTCAAGTCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAAAGCTGAC
 TACATTTTTTGGTGTCTCTCTTCTCCCTTTCCGCTGAATAATGGGTTTATGCGGGTCCCT
 AATCTGCTGGCATTGAGCTGGGGCTGGGTACCAAAACCCCTCCCAAAAGGACCTTATCTCTT
 CTTTGACACATGCCCTCTCTCCCACTTTTCCCAACCCCACTATTGCAACTAGAAAAAGTTG
 CCCATAAAATTTGCTCGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAAGGCTGGTC
 ACAACAAATCATATTCAGTTATTTTCCCTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCAGCGATGAGCGTTTCTCAGCTTTTGGAAATGCTTCCAGCTGACATCCGTTGTT
 AACCTTTTCCCACTCTCAGATATTTTTATAAAAAAAGTACCAGTGAGTTCACTGAGGGCCA
 CAGATTGGTTATTAATGAGATACGAGGCTTGGTCTGGGTGTTTGTCTGAGCTAAGTGA
 TCAAGACTGTAGTGGATTTCCAGCTAACATGGGTAGGTTTAAACCATGGGGATGCAACC
 TTTGCTTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTGGCTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGTCTCTCTTTAGAGGTCCTGGGCATTG
 ATTCCTCAATCTCAATCTTGATATGCTCTTACTGACTAAAGAGGAGAGACCTCATAT
 GGCTATTTAAATGTCACTTTTTTGCTATCCCCGCTTTTTTGGTCACTGTTTCAATTAAATGT
 GAGGAAGGCCAGCTCCTCTGACAGTACATATTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAGGTGTGTTA
 TTTTGAGTCTGAATGTACAAGCTCTGTAATCAGACAGCTTAAATACCCACACTTTTTTT
 TCGTAGTGGGGCTTTTCCATACAGAGCTTGGCTCATAACCAAATAAAGTTTGTGAAGGCCA
 TGGCTTTTACACAGTTATTTTATTTATGACGTTACTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTCACTTTGAGGCAACTAAAAAGGCTTCAACAGTTTGTATCAGTTTCTT
 TTCAGAAACACTGTGCTCTAACAGTATGACTATTCTTTCCCCACTCTTAAACAGGTGTGAT
 GTGTGTTATCTAGGAATAGAGAGTTGGCAAACTCTCTCATTGTAATAGAGTTTGTGTG
 TACTTCTCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA
 GTTTTGTGTGTCATCTGTGGCCCAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
 CCAATATGTGTGACGTACACTCATTTGTACAGGCGTGGAGACTCATTTGATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTACCCCTCTTACCAGTCAGCTGCCTGCGAG
 CAGCTATTTTTCCTAAAGTTTACAAAGTATTAGAAGTTTTCAGTTCAGGGCAAAATGTT
 ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGAAGTTGACCTGACAAAGGCAAAACA
 TGACAGTGGATTCTTTTACAAATGGAAAAAAATCCTTATTTGTATAAAGGACTTCCC
 TTTTGTAAACTAATCCTTTTTATTGGTAAAAATGTAATTAATAATGTCGAACCTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFR
LDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCCGGCTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCTCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGTCCGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
 CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGATGGGTAGTGGAGAGCATCG
 CGGGGTTCTGCGAGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCTCTTGGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAATCCT
 GAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAACAGAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG
 AATAATTTCCCAAGGGGATGGTGAACATTTTGACACCCACCCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCCTTTGGGAAGAAAAGTGAAAGGTCTGAAACTTCTCCCTCC
 CACAAAAAGCCTGAAGATTCTTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGACAGAGAACTCAAAGAAGAGTTATTATAAGTA
 ATAATTAAAGACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEEDDEVWVVESIAGFLRGPDWSIFILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVP
LVFDDEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAADFTEIFKAMMVQKNIEMLQAIIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
 TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
 TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
 GCCATTTTGTCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
 AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
 CCTGACTGCTTAAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAAT
 CCTGAGGGAAGTTCCTAGAAAATCAAAGAGGAATATGACCAGGAA

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FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTCTGAGGGAGGTAATTAAGAAAC
 AGTGAATGAGAAACAGTGTCTGTAGTCATCTGTAATATGCTCTTGTCAACAATGTATAC
 ATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCTTCTGTGTTATAAGAAAGATCATCAAAGTAG
 AAATTTGAAATATGCTTCTCGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTCGCCT
 TTTCTTTATTTCTGGATAACTTGATTGCTTCTATGTCCTGTCCATCTTCAACCAGGCCATG
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAA
 GAGGCGCTCAAACCTGGATCCAGTGGGCTTCCCTCTGACTTTATTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTTACAGCAACAACCTTGCGAGGACGTGGATTTTCATCAGCATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCCAGAAAGACAATTG
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCACTGAAAGCATCTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTTAAATGGGCTGACTCTGGGCCCTTCAGAGGA
 GTAACCGGTGATCAGATTAGAAGCTGTGGATTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTCAGGGGCTTTTCAGTGGCTTTTCATTCTGAAGTTCTCGGTGATAA
 CATGTTCCATGTCTTGTAGTGGCCAGGTACCAGTGTCTATTACACAACAGTGTCTGTGCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTGAAGCCCCATCAGTCTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTCTTGAACCTTATTTTTCACATTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATA
 AACCAGAAATGTTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTTCTAAGAAGCTGATACAGGAGTAACA
 ATATGAAGAATTCATTAAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTGTAGCTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTTACATGTTTACATGCCAAAGT
 CTTCCCTTTTAAACATTATAAAGACTAGGTGTGCTCTTGAAATTTTGAAGCCCTAGAGATAGT
 CATTTTGAAGTAAAGAGCAAGCGGACCCTTTCTAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAAATATTTTGTGGAAGAGCAGT
 TTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATGGATTTTGTG
 AATAATCTTTGATGTTTTAAACATTTGGTTCCCTAGTCACCATAGTTACCATTGATTTTGA
 AGTCAATTTAAACAAGCCCGGTGGGGCTTTTTCTCCTCAGTTTGAAGGAAAAATCTTGTAT
 GTCAATTAAGTCACTTTACAGTGTCTTACACTTAAAGAGTGCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAACAAAAGTGACTGCTCAGGGTCATGCAGTGGGTGATGATAGAGAGTGGG
 CTTTAAGTGGCAGGCTGTATGTTTACAGACTACCATACTGATGAATATGAATATGAGTTTGT
 CATTTCTCAGAACTTATACATTTTCTGCTCTCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAATG
 GTGGAATTTGTAATTAATAATATTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQ PAMAV
 IFSNFSIITTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPNSNCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFD FRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDESEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCCTAAAGGCTACTGCTGCTACTACGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGAATGGAA
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTTCAGGATAGTGTGAAGAGGCGTCTAAA
CTGGATCCAGTGGGCTTCCTCCTGACTTTATTTTGTCTATGTGGCCTTGACTGCCGGGA
CTAAAACCTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGCGGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTCGGGGCGAGGAGCAT
 CCCGCTTACCAGGTCCTCAAGCGGCGTGGCCCGCGGGTCATGGCCAAAGGAGAAGGCGCCGAG
 AGCGGCTCCGCGGCGGGGCTGCTACCACACAGCATCTCCAAAGCACTGAACGCGCCGGCCA
 GGTGAAGAAAGAACCCAAAAAGAAACAACAGTTGTCTGTTTGAACAAGCTTTGCTATG
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCCTCAGATCTAC
 CTATTG**ATG**TGGGCTCAGGTGGGCCCTTTCTCTGCCCTCCATCATCCTGTTTGTGGGCCGAGC
 CTGGGATGCCATCAGACCCCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC
 TGGGTCGCCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGTCATTGCTACTTCCCTC
 ATCTGGTTCGTGCCGACTTCCCACAGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCCT
 CTTTGAACAATGGTCAGTGTTTCCATGTTCCCTACTCGGCTCTACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTCTGGGCAC
 AGTGCTGGGACGCGCATCCAGGGACAATCGTGGGCCAAGCAGACACGCGCTTGTTCAGG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACACATGGCACCACTTACAC
 AGGGAACCGCAAAAGGCATACCTGCTGGCAGCGGGGGTCAATTGCTGTATCTATATAATCTG
 TGCTGTCTATCCTGATCCTGGGCGTGGCGGAGCAGAGAAACCTATGAAGCCAGCAGTCTG
 AGCCAATCGCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGCGCCATACATCAAACCTT
 ATTACTGGCTTCCCTTCACTCCTTGGCTTTTATGCTGGTGGAGGGGAACCTTTGCTCTGTT
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCCCATCTGGCAGTGGTTCTTGACCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTCGACGCTGCCCTTCTTAC
 TACCCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCAATTCCAT
 GGAACCGAGCCCATCTTCTTCTCTATGTCTTCTTCAACAAGTTTGCTCTGGAGTGTC
 ACTGGGCATTTCTACCTCAGTCTGGACTTTGCAAGGTACCAGACCCGTTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTTCTATCCCTG
 CTGGGCTGCTGCTCTTCAAAATGTACCCCATTTGATGAGGAGAGGCGGCGGAGAAAGAA
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCTCT**TAG**GGCCCCGCCAGTTGCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGAGGTGGCCAGGACACTTGCTGTGCTCACTGTGGGGCCGCTGCTCTG
 TGGCCTCTGCTCTCCCTCTGCTGCTGTGGGGCCAAAGCCTGGGGCTGCCACTGTGAATA
 TGCCAAGGACTGATCGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

MWLRWALSIFPSSCLWAEFGMPQSQTPTWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGGQIVGQADTPCFQDFNSSTVASQSANHTHGTTHSHRETQKAYLLAAGVIVICIYITCAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFCT
YTLGFRNEFQNLLLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIT
ITYAVAVAAGISVAAFFLLPWMSLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG
ITSLSLDFAGYQTRGCSQPERVKFTLNNMLVTMAPIVLILGLLLFKMYPIDEERRRQKKAL
QALRDEASSSGCSTDELKASIL

FIGURE 13

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCAATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCCTCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAA**ATGT**
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTATGCAATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG
 ACTTTCTATTGTGGCAAACCTCCAGAAAACAACCCCTTTTGTGTCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCTACCAAATG
 CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCATTAGCATGCTGACTTGCTCATCAGTTTTCACAGTGGCAATTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGACAGCAATGGTCTATGTCAATTTCTCTTCTTGGTTTTTCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTT**TGA**TGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTTCAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACCTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

FIGURE 15

MWWFQQGLSFLPSALVIWTSAAFI FSYTAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLVIWCGVSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNERTRLLSRDI

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FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGAC**ATG**CGCCCGCTTCTCGGCTCCTTGGTCTTTCGCCGCTGCAC
 CTTGCGCTTGTACTTGTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCCTACGTGTTCTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCATCTGTGT
 GCAGACAGGGTCCATCTGTCAACCCTAACCTCTCTGATGCTCTTTTCTCCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCTCATTAATAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACA**TGA**TCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTGTTGTAATGGA
 TGTGGTCTCTAAAGCCCCCTCATTTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTTC
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYFPDKVALLQRKVEENRNSLFFFLFLRLFPMTFNWFLNLSAPILNIPIVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKFKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCAGAGCGGGAGGAGCCCCAGGGGGCGGAGCCCCGCATGAATCATTTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACAGTGGTTTCCGAAGTCCAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTTGCC
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCATGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTCTCAGAACTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 20

MDLAANEIS IYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEFQRPPFPQYPLLIVVY
 KVLATLGLILLTAYFVIQPFSPLAPEPVLGAHTWRS LIHHIRLMSLP IAKKYMSENKGVPL
 HGGDEDRFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVM LLEDAPRKFERLHPLVIKT
 GKPLLEEEIQHF L CQYPEATEGEFSEGF FAKWWRCFPERWFFPY PWRRLNRSQMLRELFPV
 FTHLPFPK DASLNKCSFLHPEPVVGS KMHKMPDLFIIGSGEAMLQLIPPFQ CRRHCQSVAMP
 IEPGDIGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCCGTTCTTCGCCCCGGCGCAGCTGTCCCCGAGGCGGGAGGAGCCCCGAGGGGCG
CGAGCCCCGCATGAATCATTTAGTCAATCATTTTCAGTTCTCAGCCGTTTCAGTTGTGATC
AAGGGACACGTGGTTTCCGAACAGCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTTCAGAGACTGTTG
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGAAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC



FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCTGGCTGGTG
 CCCTGTGTGGCAGCTGTAGACCGTGCCTATGAGCCGCTGGGGCTGCAGTGGGGACTGCC
 CTCCTCGCCACCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA
 ACCCGAATGGCCCACTTATCGACAAACAGGTACAGCAAAC**ATGT**CCGAGTTCCGAATG
 GACACGTTATGCTAAGAGGCCAGCAGCTTATGTCAAGTTTCTGGAATGCTCTGATGACATGCT
 TATGAGCAGTGGCGAGCGCCAGTGGGAGCGGCCAGAGTCTGTGGGCGCTTCCAGGAGC
 TGGTGTGGAACCTGCGCAGAGGCGGGCGCGCTGAGGGGCTACGCTAGCAGCGCAGTGCTG
 AAGCAGCAGGCAACGCAGACTCCATGCCCCCTGCTGCAGCTGGGGGCGCTGTGGCGCAGCT
 CGCCAGGCCATGTGGGGCTGTGGCGCTGAGGGAGACTCCCATCCCCGCTGGAAACTGTCCA
 GGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGGCCACCATCTCGACCTGTGACCCCTC
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTGACACCCAGCAGGAGGC
 CTCACTGCCCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTCTGTGAGG
 AGGACCAGCTCGCGAGGACGAGCTGGCTGAGCTGAGAGCCCCGATGGAGGCACAGAACTG
 GATGAGCAGCTGAGAAGCTGGTGTCTCGGCCGAGTGCAGCTGGTACGCGTGTGGCCGCT
 GGTCCCAGGGCTGTGGAGGATCACCACACAGAATGTACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGAGGAGGCTCGGCTATGATTCCGGCGCCACTGGCCAGCTGGCCGCTGAG
 GTCACCTGCGCGCTTTCAACTGGCGCGTTCAGCACTTGAGCTCTTTATCGATCAGGC
 CAACTCTCTCACTTCCCATGCAAGGTGGGCACGACCGAGTCTCACTCTCTAGCCAGA
 CTCGAGACCCAGCTGGCCCATCCCAACCCATACCCAGGTACGGAACCAAGCTGTACTCTG
 TGGCTCTGCGGCTACGGCCCGCTCTCAAGGCTTACCTAAGCAGCGCTCCCCAGGAGAT
 GCTGCGTGCCTCAGGGCTTACCAGAAATGGGTACAGGCTGAGATATCCAATCTCGATGACT
 TGTATCAACTCAACCACTTGGGGGCGGACCTCAATGACCTGTCTCAGTACCTGTGTCTC
 CCCTGGGTCTGACGAGCTACGTGTCCCCAACCTGGAGCTCAGCAACCCAGGCGGTCTCCG
 GGACCTGTCTAAGCCATGGGTGTGGTGAACCCCAAGCATGCCAGCTGTGAGGAGGAAGT
 ATGAAAGCTGTGATGACCCAGGAGGACCATTGACAAGTTTCACTATGGCAACCCACTACTCC
 ATGGCAGCGTGGAGGCTGCTCACTACCTCATCCGCGTGGAGCCCTCACTCTGCTGACGTCCA
 GCTGCAAGTGGCCGCTTGTACTGCTCCGACCGGCGAGTTCACCTCGGTGGCGGCGAGCTGGC
 AGGCGATGTGGTGTCTACCCCGTGGGCGAGCTCTCCTGAGGACTCATCCCGAATTTCTTACTTCT
 GACTTCTCGGAGAACCAACAGCTTTTGCACCTGGGCTGTCTCCAGCTGACCAACAGGAGAGGT
 AGGCGATGTGGTGTCTACCCCGTGGGCGAGCTCTCCTGAGGACTCATCCAGCAGCACCGGC
 AGGCTCTGGAGTCTGGAGTATGTGTCTGCACACCTACAGCAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCGAGGAGGCCCTCAATGTCTTCTATTACTGCACTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCCTGTGACAGTGTGAAGGAGCCACATCCAATCGGCTGTCA
 GCTGAGGAAGCAGCCCATCGCTTGCACGCTGGACACTAAGTCACTAGCATCTTCCAGCA
 CCTGGACGAACCTCAAGGCATTCTTCGACAGAGGTGACTGTGAGTGGCAGTGGGCTGTCTGGGCA
 CCCACAGCTGTGTGCCCTATGACCGCAACATAAGCAACTACTTTCAGCTCAGCAAAAGACCCC
 ACCATGGGCAAGCCACAAGACGACGAGCACTGCTGAGTGGCCGCTGGGCTGCGAGGAGTGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCGGATGGAAGCTGCTATTACGCGGTGGCCACTGGG
 ATGGACGCTTGGGGTGTGCTCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGTAGTAACCTGCCTTGCAGTGGACCACTGTGGCATCTACCTCATCTCAGGCTCCCG
 GGACACCACTGCATGGTGTGGCGGCTCCTGCATCAGGCTGCTGTCTGAGTAGGCTGGCAGC
 CAAAGCTGTGCGAGCTCTGTATGGGATGGGGCTGACGTGAGCTGTGTGGCCATCAGCACT
 GAACCTGACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATACACATGTATACGCG
 CGGACAGTTTGTAGGGGCACTACGGCTCTGGGTGCCACATTCCTTGGACCTATTTCACAC
 CAGGATTGGGTCTCGAAGGCCAGATTGTGGTACAGAGCTCAGCTGGGAGACGCTCTGGGGCC
 CAGTCACTACTCTTGCACCTGTATTGAGTCAATGGGAAGTTGGCGGCTTCACTGGCCCC
 TGGCAGCAGCTCTGACGCTGACGGTGCAGAGGACTTTGTGTGTCTGGGACCGCCAGT
 GCGCCCTGACATCTTCAACTAAACACACTGCTCCCGGCGCGCTCCTTCTGCCATGGAAG
 GTGGCCATCCGACGCTGGCTGACCAAGGAGCGCAGCCAGCTGTGGTGGGCTGTGAGGA
 TGGCAAGCTCATCTGGTGGTGGCGGGGCGAGCCCTGTGAGGTGCGGACAGCCAGCTGTGGCG
 GGAAGCTGTGGCGGCTCTCGCGCGCATCTCCAGAGTCTCGGAGAGACGGAATACAAC
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGCTGTCTGGGCCCCCGCCCCCGAGGCGT
 CGCGGGAGCCGCCAGCTGAGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG
 GCGGGAAGTCCCGCCCTCGCGGCTGAGGGGCGCGCTGAGGGCCAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDMLSGFWNACYDMLSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLQQAATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSAETYSRMLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRSSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRPQEMLRASGLTQKWVQREISNFYEYLMQLNTIAGRNYNDL
 SQYPVFPWWLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSCDRQFHSAVAWQARLESPADVKEIP
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVLPWPASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYCTYEGAVDLDHVTDERERKALEGII SNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLD TNPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWWPGSGVSGQALAVAPDGKLLFGGHWGDSLRTVLPALPRGKLL
 SQLSCHLDVVTCALDTCGIYILISGSRDTCMVWRLLHQGGSLVGLAPKPVQVLYGHGAAS
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGQIVVQSSA
 WERPGAQVITYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAAATCATGGGGTCTTGGGGCTCTTC
 TGGACCCCTTAACCTGGGTACTGGCCCTGGGCCAATGCGTCTCTCGCTGGAGCCCTTGGCTCCTT
 CTACTGGGCCCTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTCTGCTGGACAAAGTCACAGA
 CCTGCTGCTGTCTTTGGGAAGCTGCTGGTGGTTCGGAGGCGTGGGGTCTCTGCTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTTGCCATCATGACCTCCATCCTGGGGGCTTATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTCGGCATGTGTGGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGGGCCCCGGACAACAAGAAGAGGAAGAAG**TGA**CAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTTTAGGCCAGGCGCGGTGGCTCACGCCGTGAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGAAGGCATGCACCTGTCATCCAGCTAC
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTGTGTTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLGLF
 WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFFPLISAFIRTLRYHTGSLAFGALILTLVQ
 IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
 NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGVGVLSTFFFFSGRIPGLGKDFKSPHLNYY
 WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGLDRPYYSKSLIKILGKKK
 EAPPDNKKKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT
 GGCTATGTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC
 CAGTGTGACCGCTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG
 CCAGTCAATGTGTCATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGATGGGTGACAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCGCGGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTCGCAGCG
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCCTTGACAGCATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
 AGGCCATGGACATCTCCTTGAAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACACTTTCAGCATTCATTTGGGTTCAAGCACAAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
 CTTTGACCAACCTCGTCATCTCCAGGGGCCCTTTCCGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCCCTTTGTGTGTTGACAAAGAACCGGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCAGTGAACGCTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAAGCTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAGCACCAGCTCCCGGA
 TGCTGCACAACCAATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCACTTATTTCCCTCCTGTCTCTAGGAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAACCTGGCTTTCATTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPEDDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAIEDIFRDEEEDDEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNNHFDLSVIELKAEDRSKFL
DALISLLS

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FIGURE 28

GTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

CGAGAACCTCTCTCTTGGCTCTGGATTGGGAGCCCTTTCCAGTACCATTCTCTAGTGAAAC
 CACGAGGGCAGCATACCAAAAAACCCCTCAACCCCAAGGAATAGACTACAGGCCCAATTTG
 GCTGACTTTGGCTATAGAAAAAGAAAGGACGAAAGAGACAGTTTTTTTTGGAAAGCTAA
 GCTCTCCCTTTATCGAGTCAAGAAACCCGCCCTCTCTGAGCTATTTACAGCTTTTAAACAT
 GAGTAAAGTACGCTCCCGGTCAAC**ATGGT**GACAGCGCGCTGGGTCCCGCTCTGGGACGGCTC
 CTGCTCTTTCTCTCTGTGTGAGTACCGTATGTGTGGAGCTACCTTTACAGAGCTCTGGCC
 CTGCTCTCTCTACAGCGTGTGTGACTTGAGGACCCCTGGATCTCGCCATGTATCTCCAG
 CCTCTTCCTCCGCCGCCCCACGCCCTGCTGAGATCAGACCCATACATTAATATCACCAT
 CTGAAGGGTGCAAAAAGGGGACCGAGCCCAATGGGCGCTCGAGGTCATGGGCGAGGGGG
 TCCCAAGAGGGGACCTGGCCCTCAGGCGCAGCAAGGTTGACACAGGGGAGATGGGCGAGCCCG
 GCGGCCGGTCTCAGAAGCGCTTTTTCGCTCTCTCAGTGGGCGCAGACGGCCCTGCACAGC
 CGGGAGGACTCTCAGACCGCTGCTCTCTCAAAAGGGTCTTTGTGAACCTTGAGTGGGTGGCTTGA
 CATCGCAGCGGCGAGTTTGTGCTTCTCCCTCGTGGTCATCTACTCTTCAGCTCAATGTGG
 ACACATCGAATTAACAAGAGAGCTACGTGCATCATATGATCAACAGAAAGAGGGCTGTCACT
 CTGTACAGCCAGGCGACGAGAGCGAGCATCATCAGAGAGCCAGTGTGATGTGCACCTGGCC
 CTACGGGGACCGGCTCTGGGTGGCGCTCTTCAAGCGCGAGCGAGAACGCATCTACAGCA
 ACAGCTTCGACACCTACATCACTTTACGGCGGCACTCATCAGGCGCGAGGACGAC**TGA**GGC
 CTTCTGGGCGGCTCCCGGCTGGAGAGCTCAGGTGTGGTCCGCTCGGCTCGAGGGGCTCAG
 TTTCGAGCTGCTTGAAGCAGGAAGGCGAGGAGGTCTCCCGGGGACCTGGCAITCTGGGGAGG
 TTTCTGCTCTCTATCTGGCTGCTCATCTCCCTCCAGGCTATTCTGCTCTCTCTCTCTCTCT
 TGGACTATTTTAAGAGCTTGCTTACCTAAATTTCTAGAATCTTCCGAGCTCTGTAGGCC
 AGACTCTTCAACTTGGAAATGCTATGCGAATACCCGGGGTTCGTGTAAATGCGAGATTCT
 CACTCAGCAGGCTATGGATGGGTCTCAGGATCTGTGTTCTCATATGTCTCGGGTGTAGTCTG
 ATGGTCTACGCTCATGAACCACTGAGACCAAGGCTCTAGAGCTTTCTCAATATTCTCTAG
 TATCTTCTGACATCTTGAATTTGACCGCCCACTTCTAGAATTCTCCAAACATTTTTTTCTCT
 TGAATCTGCTCTTGTGTTTCCGAGGAGAGAGTGGAGTGTGCAATCTCAGTTCACCTGAC
 AACCTCTGCTCCCGGTTCAAGGCTTTTGTGTTGTCAGGCTCTCTTGTGGTGGGATCTG
 AGGCGCTCTCTACCATCTGCTTGTATTGTGTTTGTATGATAGTATGGGTCTCACCATTA
 TTTGGCCAGGCTGCTGTGAATCTGACTTTCTAGGTGACACACAGGCTCTGGGCTCTCAAAAT
 CTTGGGATTCAGGTTGAGGCCACGAGTGGCTGTCTCTTCTCAACATCTTAAATCTCTCATCT
 CCCCCTCAGGGCTCCCGGTGCTATGTTCTCTTACCGCTCTCTCTCTCTCTCTCTCTCAGG
 TGCACCACTGCAGCCACCCTTCAATTTATTCATCTAAACACTGAGCACTCACICTCTCTCT
 GGGTCCCGGGAGGGTGAAGGGGTGCAGACAGGGCCCTGCCCTGCCCTCAGTACTGCTCC
 GTCCAGCCAGGCGGGGAGAGATGTGTACATAGGTTTAAAGCAGCCAGGACTCATGGCG
 GCTCTGTGTTCTGGGTGTTTCAGGTGCTGTGTGTCTCTCAATTACCACTGCTCTCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGCGAGGGGAGGTATCTCTCTCCGTTCTCATCCACTCTGCCAC
 TGCTCATCTGTTTACAGCAAAACCCGAGGGGCTTGCCAGGCTCAGAGGTTCTGTGAGGAGAGG
 ACCCAGGAGTGTGGGGCATTTTGGGGGCTGAAGTGGCCCGGCAAGAAATGGAACCCACACCA
 TAGCTCTCCCCACGCTCATACGGATCTGCGAGAAGACTGCCCTCTCTCATGGGATCCC
 CTTCTGCTCTCTCCAGGGGCTTGCCAGGGCCTTGCTCAGTCCCTCTACCAAACTCATCT
 GAATTTCCGTTTCCCCAGGGGCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCAAGTGCT
 CTTCTGCCCTCATGTCCCTCTCACGGCCGACTGCCCGCACTTCCAGGCTTTATCAAGTGT
 CTAAGGCCCGGGTGGGACGCTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCTTTTGA
 AAACACTCTCAGAGAAGGGCCACGAAGCCCGAGGCTTTAGAGCCTCAGCAGGTCTTGGG
 AGTCTAGACAAAGGAGGACCTCAGGCCCTTCGTTTCTCTTCCAGGTTGGGTTGGCTGGTGG
 GTTCCCTTAGCCTTTCAAACCCAGGTGTGGCTGCCCTCTCCCAAGGAGGAGCGGCTCCGC
 CCAATTTGGTGCTATCGACACTCTGGGGCTGAGGTGCCACCGGGGGGTGATCTCTGTGCTCAC
 AGCGGAGGACGCGTGGTCTCATGGCCAGATGACGGAACAGGCTGTGACACAGTGTCCGAGA
 AGACTGTGTCTATAAACACCTCTGCTGATCTGCCCTGCCCTGCCCTGCCCGCCAGCCCTGCC
 GTTCAGCATGATTAAAGATCTGCTCTCTCTTGTGAAAAAAACAAAAA

FIGURE 30

MVTAALGPVWAAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

ACTCGAAGCGAGTTGCTTCGGGACCCAGGAACCCCTCGGGCCGACCCGCCAGGAAAGACTG
AGGCCGCGGCCTGCCGCCCGCGGCTCCTCGCGCGCCGCGCGCTCCGGGACAGAGCAG**ATGTG**
TCCAGGGTCCCTCTGCTGCTCGCGTGTCTGCTGCTGAGCCCTGGGCGCTGGGGTGAGG
GCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
ACCACGGTGCCCGAGAGCTGCCACCCGACAGCTGGGGCTGTAGCTCTTTGAGAACCGCAT
CACCATTGCTGCAGCAGCAGCTTTGCGGCGCTCGCGGCGCTGACGCTCTTGACCTTGCTAC
AGAACAGATCGCCAGCTGCCACGGGGGTCTTCAGGCACCTCGCCAACTCAGCAACCTG
GACCTGACGCGCAACAGGCTGCATGAATACCAATGAGACCTTTCGTGGCTCGCGGCC
CGAGCGCTCTACCTGGGCAAGAACCGCATCGGCCACATCAGCCTGGTGCTTGACACGC
TCGACCGCTCTTGAGAGCTCAAGCTGCAGGACAGCAACGAGCTCGGGCAGCTGCCCGCTGCGC
TGCCCCGCTGCTGCTGCTGACCTCAGCCACAACAGCTCTTGCCCTGGAGCCCGGAC
CCTGGAACATGCCAACGTGGAGGCGCTGCGGCTGGCTGCTTGGGGCTGCAGCAGCTGGACG
AGGGCTCTTTCAGCGCTTTCGCAACCTCCAGCAGCTGGATGTGTCGCACAACTGAGTGGAG
CGAGTGCCACTGTGATCCGAGGCTTCGGGCGCTGACGCGCTCGGCTGGCCGCAACAC
CCGATCTGCCAGCTCGCGGCCGAGGACCTTGGCCGGCTTGGCTGCTCGAGGAGCTGGATG
TGAGCAACTTAAGCTCGAGGCGCTGCTGGCAGCTCTTGGGCTCTTCCCGCTCGCG
CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGTTTGGCCCTG
GGTCCGCGAGAGCGCTGCTCACTTGCCAGGCTCTGAGGAGAGCGCTGCCACTTCCCGCCCA
AAGACGCTGGCGGCTGCTCTTGAGAGCTTACTACGCGACTTTGGCTGCCAGCCACCC
ACCAAGCCACAGTGCACCGACAGCGCCGCTGCTGCGGGAGCCACAGCTTGTCTTCTAG
CTTGCTCTCTACTGGCTTAGCCCCAGGCGCGGCCACTGAGGCCCGCCGCTCCCTTCA
CTGCCCAACCGACTGTAGGGCTGTCCCCAGCCCGAGACTGCCAACCTTCACTGCTCT
AATGGGGGACATGCCACTCGGGGACAGGCGACACCTGGGCTGCTTGTGCCCGAAGGCT
CACGGGCTGTACTGTGAGAGCAGATGGGCGAGGGGACAGCCGCAAGCTTACCAAGTCA
CGCCGAGGCCACAGCTCTCTGACCTGGGCATCGAGCCGCTGAGCCCCACCTCCCTGCGC
TGGGGCTGCAGCGCTACCTCCAGGGGAGCTCGGTGCAGCTCAGGAGCTCCGCTCCCTACCTA
TCGCAACCTATCGGGCGCTGATAAGCGGCTTGTGACGTGCGACTGCTGCTGCTGCTGCTG
AGTACAGCGCTACCCAGCTCGGGCCAGCAAGCCACTTACTCGCTCTGTGTATGCTTCTGGG
CCCGGGCGGGTCCGGAGGCGAGGAGGCTCGGGGAGGGCCCATACCCCCAGCGCTCCA
CTCCAACACGCCCCAGTCAACCAGGCCCGCGAGGGGCAACCTTCGCGCTCCTATTGCGCCC
CCCTGGCCGGGTGCTCTCGGCGCGCTGGCTGCGGTTGGGGGACGCTATGTGTGCGCGG
GGGCGGCTCATGCGACAGCGCTCAGGACAAGGGCAGGTTGGGCGAGGGCTGGGCGCT
GGAATCGAGGGAGTGAAGGTCTCCCTTGTAGGACAGGCCCGCAAGGCAACAGAGGCGGTGAG
AGGCCTGCCAGCGGCTGTAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCGCTGGGCTC
CAGTCAACCTCCAGCGAAAGCCCTACATC**TAGG**CCAGAGAGAGAGGCGAGCTGGGCGG
GGCTCTCAGGACAGTGAGATGGCCAGCCCCCTCTGCTGCCACACCACTGAAGTTCTCAGTGC
CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCGTCTCCCTCTGGA
CCTCGGCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC
CGAGTGCCCTATGAGGACAGTGTCCGCGCTGCCCTCCGCAAGTGCAGTCCCTGGGACGCGG
GGGCTGCATGTGCTGTGTAAGCATGCTGGGTCTGCTGGGCTCTCCACTCCAGCGGA
CCCTGGGGGCGGCTGAAGGAAGCTCCCGGAAGACAGAGGAGAGCGGTTAGCGGCTGTG
TGACTCTAGTCTTGGCCCGAGGAAAGCAGAGAACAGAAAGTGAAGAGGAGATCTTTA
GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTATTCTG
GGAAGATGTTTTTCAACTCAGAGCAAGGACTTTGGTTTTTGAAGACAACCATGATATG
AAGGCGCTTTTGAAGAAAAATAAAGATGAAGTGAAGAA

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDPVPDPTVGLYVFEN
 GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLDLSHNSLLALEP
 GILDTANVEALRLAGLGLQQLEGLFSRLRNLDLHDLDVSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
 PWVRESHVTLASPEETRCHFFPKNAGRLLLELDYADFGCPATTTTATVPTRPVVREPTALS
 SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPQPDQCPPSTCLNGGTCHLGRHHLACLCP
 GFTGLYCESQMGQTRPSPPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSSVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRGRAMAAAAQDKGVGPGAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFFPGPLQSPHAKPYI

100
 90
 80
 70
 60
 50
 40
 30
 20
 10
 0
 100
 90
 80
 70
 60
 50
 40
 30
 20
 10
 0

FIGURE 33

GAATCATCCACGCACTGCAGCTCTGCTGAGAGAGTGC AAGCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAACTCCTTGGAAATACAATGAGACTCATCAG
 AATCATTTACATATTTTGTAGTATTTGTTATGACAGCAGAGGTGATGCTCCAGAGCTGCCAG
 AAGAAAGGGAACTGATGACCAACTGCCTCAACATGCTCTCAAGAAAGGTTCCCGCAGACTTG
 ACCCGACCAACAGCACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTTCAGA
 TTTTTCATTCTGTCTCAAACTGAGAGTTTTGATTCATGCCATAACAGAAATCAACAGACTGG
 ATCTCAAAACCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTCTTTAATGACTT
 TGACACCATGCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAAATACAAAATCAGATTTCCGAGAAAATGCTCATCTGCATCAAAATACTGTC
 TTCTTAGAGTTCAAGAACTCTTCTCATTATGAGGAAGGTAGCTGCCCCATCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGACACAAATTTCTGGGTTCTTTTGGGTGATGGAATCA
 AGACTCAAAAATATTTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTGA AAAATGCTTAAGACATCGGTTCTATTTGCTTAATAAAGTTGA
 TTTACTCTGGGACGACCTTTTCCCTATCTTACAAATTTGTTTGGCATACATCAGTGGAACTCT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTTCAATTTGACTAC
 TCAAAATCTGTAATGAGAATAATAAAATTTGAGCATGACATTTCAAGGTATTTTACATTC
 ACAGGATAAAATCTATTGCTTTTGGACCAAAATGACATAGAAAACCTGACAAATCAAAATG
 CCAAAATGCCACACATGCTTTTCCCGAATATCTCAAGAAATCCAAATTTAAATTTTGGC
 AATAAATATCTTAAACAGACGAGTTGTTTAAAAGAATCTCAACTGCTCACTTGAANAATCT
 CATTTTGAATGCCAATAAATCGAGACACTTTCTTTTGAAGTTGCTTTGCTAACAACACAC
 CTTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAAATAAAATGATGAAATTTGCTCA
 CGGCGAGAACTGTGGTCAATGAATCTGTCATACAAATAAATTTGCTGATTTCTGCTTCAG
 GTGCTTGCCCAAAAGTATTCAAATCTTGACCTAAATAATAACCAATCCAAACTGTACTCTTA
 AAGAGACTATTCATCTGATGGCCTTACGAGAATCAAAATTTGAAATTTCTTAACTGAT
 CTCCTCGGATCGAGTCATTTCACTAGACTTTCACTTCTGAACATTTGAAATGAACTCATCT
 CGACCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCAATGCGGGAAGAA
 ATCCATTTCCGGTGTACCTGTGTAATTTAAAAATTTTCACTCAGCTTGAACATTAATTCAGAGT
 ATGATGGTTGAAATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGCAACTAG
 GTTAAAGACGTTCACTCTCCACGAATTTATCTGCAACACAGCTCTGTGTTGATTTGCACCAT
 TGGTTTATTATGCTAGTTTCTGGGTTTGGCTGTGGCTTCTGCTGCTCCACTTGTACTGCCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCAGAGGTTAGGAACAAACACCCA
 AGAACAACCTCAAGAGAAATGTCCGATTCACGCAATTTATTTATACAGTGAACATGATTTCT
 TGTGGGTGAAGAAATGAATTTGATCCCAATCTAGAGAAGGAAGATGTTTCTATCTTGAATTCG
 CTTTATGAAAGCTCACTTTGACCTGGCAAAAGCATTAGTGAATAATTTGAAGCTTCAATGA
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCAACCTTTGTCCAGAATGAGTGGTGCAAT
 ATGAATTTACTTTTGGCCACCACAATCTCTCCATGAAAATTTGATCATATAATTTCTTATC
 TTAAGTGAACCCATTTCCATTTCTATTGCAATTTCCACAGGATATCATAACTGAAAGCTCTCT
 GGAAAAAAGCATACTTTGGAATGGCCAAAGGATAGGCGTAAGTGTGGGCTTTTCTGGGCA
 ACCCTTCGAGCTGCTATTAAATGTTAATGTATTAGCCACCAGAGAAATGTATGAATCGAGACA
 TTTACAGAGTTAAATGAAGAGTCTCGAGTTCTACAATCTCTGATGAGAACAGATTTGTCT
 ATAAATCCCAACAGTCTCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATA
 CAACCTTTATGATGGCAATTTGCAAAATTTATTAATAAATAAAATGGTTATTTCCCTCATTA
 CAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTCAAGATTTTATAAGG
 GCTTTATGAAAAGGTTGTTCTCCAGGATTTTATAATCATGAAAAATGTGGCCAGGTGCG
 AGTGGCTCACTCTGTGAATCCAGCACTATGGGAGGCCAAGTGGGTGAGCCACGAGGTCAA
 GAGATGGAGACCATTTGCTCAACATGGTGAACCCCTGTCTACTATAAAATCAAAAATTTA
 GCTGGGCGTGTGTTGTCACGCTGTAGTCCGAGCTACTTGGGAGGCTGAGGCAGGAGAAAT
 CTTGAACCCGGGAGGTGGCAGTTGCGATGAGCTGAGATCGAGCCACTGCACTCAGCTGCTG
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAATGAAAAACATCC
 TCATGGCCACAAAATAAGTCTAATTCATAAATTTATAGTACATTTAATTAATTAATATTA
 CATGCCACTAAAAAGAAATAAGGTAGCTGTATTTCTGGTATGAAAAACATATTAATAT
 GTTATAAATCTATTAGGTTGGTGCAAAACATAATTTGGTTTTTGGCAATGAAATGGCATTGA
 ATAAAAAGTGAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTTGA
 TTACAGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATGGTTAGAATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCTT

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FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRVLDL
SFNDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFILILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTAKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENCSPETVVMNLSYNKLS
DSVFRCLPKSIQILDNNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTQTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSI FVLSFNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLEFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCCTCCAAGGACCGGCTCGGAGGGGTCGCCGGGAAAGG
 GAGGGAAGAAGGAGGGGGGGGGCGGCCCTCGCCCGCCGCGCCGCTCTCGCGCCGCTCTCGCCGCGCCGCGG
 CCAGCCACAGCCCGCGGGGGGGGCTGACACGCGCAGCCAGCCGCGCGCTCCCGCGCCAAAGAGGCGCGCT
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCGCGAGCCGCCCGCGCGCCCGGCTGACCGTGA
 CCTCTGCCCTGGGCGGGGGCGGAGCAGGCA**ATG**CCCCGCCGGGACCGCTACCCGAGCCGCTGGCCCTGTGTCT
 CTGCGCAGTGACCTTGGCGGGGCTCGGAGCCAGGGCGCAGCCCTCGAGGACCTCGATTATTACGGGACAGAGAT
 CTGGAGCCGGGAGCCCTACTACGCGCGCCGGAGCCCGAGCTCGAGACCTTCTCTCCGCGCTGCTGCTCGGGGG
 CCGGGGAGGAGTGGAGCGCGCGCCCGCAGGAGCCAGGCCCGCCAAAGAGGGCCACCAAGGCCAAGAAAGCTCCC
 AAGAGGGAGAAGTCGGCTCCGGAGCCGCTCCACCAGGTAAACACAGCAACAAAAAGTTATAGAGAACCAAGAG
 CTCTGAGAAGGCTGCCACGATGATCACAGTGTCCGTGTGGCCGTGAAGATGTGAGAGAGAGTTGCCACCTC
 TTGGTCTGGAACCTTAAAAATCACAGACTTCCAGCTCCATGCTCCACCGTGAAGCGCTATGGCCCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAAATGATTTTATGACGGAGCGTGGTGGCGGGGAAG
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGCGCGCTGACCAGATTCACTGGTGTATCATCAAGGGA
 GGAACCTCCCTCTGGCTGAGTGACTGGTGACATCCTATAAGGTCATGGTGAGCAATGACAGCCACACGTTGGGTC
 ACTGTTAAGAAATGGATCTGGAGACATGATATTTGAGGGAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT
 ACCCGTCCCCATGGTGGCCCGCTACATCCGCATAAACCTCAGTCTGGTTGATAATGGGAGCATCTGCATGA
 GAATGGAGATCCTGGGCTGCCACTGCCAGTCTCAATTAATATTATCACCGCCGGAAGCAGATGACCACTAT
 GATGACCTGGATTTTAAGCAACCAATTAAGGAATGCGCCAGTTGAGTGAAGTTGTGAATGAAGTGTGTCC
 CAATATCAGCAGAAATTTACAACATTTGAAAAAGCCACCAGGGCTGAAGCTGTATGCTGTGGAGATCTCAGATC
 ACCCTGGGAGCATGAAGTCGGTGAGCCGAGTCCACTACATCGCGGGGGCCAGCGCAATGAGTGTCTGGGC
 CGGGAGTGTGCTGCTGCTGTGGTCAAGTTCGTGTGTGAGGAGTATTTGGCCCGGAATGCGCGCATCGTCCACCT
 GGTGGAGGAGACCGGATTACGTCCTCCCTCCCTCAACCCGATGGCTGCGGAAGGCCATCGAAGAGGCGCT
 CGGAGCTGGGAGCTGCTCCCTGGGACGCTGGACCCAGCATGGAATGACATCAACCAACCACTTCTCTGATTATA
 AACACGCTGCTCTGGGAGGACAGGATCGACAGAAATGTCCCAAGAAAGTTCCCAATCAATATTGCAATCCC
 TGAGTGGTTTCTCTCGGAAAATGCCACGTTGGCTGCCGAGACGAGCAGTCTACAGCTGGATGGAAAAAATCC
 CTTTTGTGCTGGGCGGCAACCTGAGGGCGCGAGCTGGTGGTGGTATCCCTACGACCTGGTGGCGGCTCCCC
 TGGGAAGACGCAAGAACACACCCCCACCCCGATGACCACGCTGTCGCTGGCTGGCTACTCTATGCTCCAC
 ACACCGCTCTGACAGACGCGGAGGAGGGTGTGCCACGAGGACTTCAGAGAGGAGGAGGCATGTCAT
 TGGGGGCTCCTGGCACGCTGCGTGAAGTCTGAACGATTTCAGCTACCTTCATACAACTGCTCCGAATCTG
 TCCATCTACGTGGGCTGTGATAAATACCACATGAGAGCCAGCTGCCCGAGGATGGGAGATGCTCCGAACTG
 TCTGATCGTGTTCATGGACAGCTTTCATCGTGCATTAAGGCTTGTGAGAGATTCATCTGAAAAGGAATCC
 CAACCGCCATTATCTCCGTGAAGGCATTAAACATGACATCGAACAGCCACAGATGGGATTACTGGCGCTC
 CTGAACCTCCGGAGATATGTGTGTCAGCAAGGCCGGAAGTTTCACTGCATCCACAGAACTGTATGGTTGG
 CTATGACATGGGCGCCCAAGGTGTGACTTTCACATCTAGCAAAACCAATGCGCCAGATCCGAGAGATCTATGG
 AGAAGTTTGGGAAGCAGCCCTGAGCTTCCAGCTGAGGCTGCGGGGGCGGAAGAGACGACAGCGCT
 GGG**G**ACCTCCTGGGCCCTTGAGACTGCTCTGGGACCATGCAAAATTAACCAACCTGGTAGTAGCTCCATAG
 TGAGCTACTCACTGTGTTTCTTCTGTAATCAGAAGTGCTTGAAGAGAGGCTGCAATGTGAGGCGAGGTTCC
 CAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTCTTTGTTCCCATTTATCCAAATACTTGGACAGAGCA
 CGAGAGAAAGCTGATGGGAGTGGAGAACTCAGCAAGCCCAACCTGAGGAATCAGAGAGAGGAAGGAGAGG
 GAGCTCTGCGTTAGAGCCTTGGCTGCTAGAAAAGGATTCTGTTGCTTCCCTGTTTGGCTGGCAGCAAGG
 GTTCCAGTGCATTTGCAATTCAGCTGATTAATTTGAGCTTCCAGCTGGGCTGGGCTGCCAAATGTTACCA
 TTTGAGATGCTCCGAGGCTCCTAAGAGAATCCACCTCTCTGCGCCCTGGGACATTCGAAGCTGCTACAAATAA
 ATTCTGTGTTCTTTTGACAAATAGGCTCATTGCCAAGTGACATCAGTAGAGCCTCTGATCTGTTTAGTCTCTCT
 TTTTCAACAAAGGAGTGTGTTAGAAAAGGAGAGAGGCTGAGATCTCAGGAGTTTGTGGGCGAGCAAGCA
 TGGGCTCTTCTGCAAAATCTGGGTCATAAAACACCCCAAGTCCCTGCTGAGGATTTGCCCTGGAGGTT
 CCCCAGGTAGGAGAGCCAGAGGTCGCCACCTTCTGAGGGGCCAGAAATTTAGCCTGGATCTCCTCTTTTAC
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGCTGGCCTGAGGCTCTCTGCTGAGGATTTGCCCTGTGTG
 GAATTAGTGTCTCATGGTGGCTCATATCAGCTGGGAGTTATTTTATGATGTAGAATGCCAGATCTCCA
 GATTAGGCTAAATGTAAATGAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAATTAATGTAATAT
 CTTGCAAGAAAAAGTATGCTCACTTTTGTAAATGTTGCTGCTCATTGACCTGGGAAAAATGAAAAA
 AATAAGCCAAATGGTAAGACCTTAAAAA

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEFELETFSPPLP
AGPGEEWERRRQEPREPPKRATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPLLGETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPEGEHEVGEPEF
HYIAGAAGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSPNPDGYEKAYEGG
SELGGWSLGRWTHDGIDINNNFPDLNTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGI PNAIISVEGINHDIRTANDGDYRLL
NPGEYVVTAKEGFTASTKNCMVG YDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRQRG

CTAAGAGACCAAGTGGAGCTGGCGCTCTCATTTCTCTAGCCCTCTGTCTTCTTGGCCAAGCTGCAGGGG
ATTPTGGGGATCTGGAGACTCCAAATCCGACCCCGGCTCAGCTCTTCCCGAGTGTTGACTCCAGCTCCGTT
TTCAGCTCCAGCTCCAGCTGGGCTCCAGCTCCAGCGCGAGCTTAGGCAGCGAGGTTCTGTGTCCAGGTTGTG
TTCCAAATTTCCCGGCTCCGTGGATGACCTGGGACCTGCGAGTGTCTGTCTTCCCTCGGCAGACACACCTTT
CCGTGGACAGAGCTGGACGCTTGGAAATCAGACCTCATGTGTTCTCAGAAGTTTGGAAAAGAACTTTCAA
GTGAGGGAATATCTTCCAAATTAATTTAGTGTGTGTGAAAAGAAAGTGTAAAGCTTAAGCTTCGGAATGCATCAT
GGAGAAGATGATCAATTTCTTACCTGAATCGACTCGAGCTGATCAAGAGTAGAAGTGAAGGAGATGGAAAAAC
TGCTCATACAGCTGAAGGAGAGTTTGTGGTGAAGCTCAGAAATTTGTGCACGCTGGAGTGGAGATAGAAAT
ATGACTCTTGTGTGAGAAGACTTGAGACATGACAAAAACAATGTCTTCCATTCGCGGAGAAATGCTGGC
TCTGAAGACCAAGCTGAAGAGTTGTGGGCCCTCAAAGATCAAAACACCCCTGTGCCTCACCTCTCCACCT
CAGGGAGCTTGGTCACTGGTGTGTGGTGAACATCGAACCACTGTGTGGTTTCACTCACTGGAGAGGGTTT
TCTTTATCTATGTGCTTGGGGTAGGATTACTCTCCCGACCTCAAAACAAGGACTGTAATTTGGGTGGCGCC
ATGTAACAGATGGAGAGACTGTTGGAGTAATAGACTACACAACATGATGATTTCGATTGTATATAAT
ATGCTCGAGATGGCGGACTCACTATGCGCCAGTAGTGATGTCACAGGTTTACAAACAACACTGTACGTCAAC
ATGTACACACCCGGGAATATTCGAGAGTTAACTGCACCAACAGATTTGCTGTGACTCAACTCTCCCTAA
TGCTGCCCTAATAACCGCTTTTATCATCTGTAATGTCTTGGCAAGATTAAGTACTTGTGTGGATGAGAAT
GATTGTGGGTATTATTCAACTGAAGCCGACCTGGTAACATGGTGATTAAGCAATCAATGACACCACT
CAGGTGCTAAACACTTGGTATAACCAAGCAGTATAAACCATCTGCTTCAACGCCCTCACTGGTATGTGGGGTCT
GTATGCCGCCGCTACTATGAACACAGACAGAGAAGATTTTACTATATGATACACAACACAGGGAAGAGG
GCTAACTAGACATGTGTAATGCATAGATGACGAAAAAATGCAGAGCAATTAATCTAAACCCCTTTGACCAAAAA
CTTTATGCTCTATAAGTATGCTTACCTCTGAATTTGATCTTCTGTCTCGAGAAGCGAGTAAAGCTGTATA
GGAATTAGGGTGAAGAGAGAAATGTTTGTGGAAGAAATAGTCTTCTCCACTTATAGATATCTCGAGGGGTGT
CTAAAGAGTGTTTCATTTCGACAAATTTTAAAGTGAAGTTCTACACACTAGAGATCTAGGACATTTGTCT
TGATTTGTGTGAGTTCTTCTTGGGAATCATCTGCCCTTCTCAGGCGCATTTTGCATAAAGTCTGTCTAGGGTGGGA
TTGTTGAGAGTCTAGGGGCACTGTGGGCGCTGTAAGGCTACTGTTGAGGAGGCTCACTAGAAGCCCTTAATA
GGAATTAAGGAACTTAAAGCTCAGTATGGGCTCTAGGGATTTCTTGTACAGGAATATTTGCCAATGACTAGTC
CTCATCTCTATGACACCACTAAATTTCTCATGCTCGGAGAAGAACTGGGAGCTTAGTTAGTGAGTAAATATCT
GGAGTCTCTCGAGGAGGCAAAATCTCCAATCTTTTCTTCCCTCATAGCAGCACTGGAATAGATGTTTGTGTGG
CAGACTGAGTAAATTTGGCATGCTTATATATCTACATCTGTAAAGTGTCTGAGTTTATGGAGAGGACCTTTT
ATGCATTAATTTTACATAGGCAAAATTAATCCAGAAGGATCTGTAGATAGGCAAGCTGCTTTTCTTTCTCTC
ATTGTCCACCTTACATAAAGTCAGTAGAATCTTACTCTATAACTTCTCTCAAAGCGAGCTCAGAGAATAG
AACCAGACTTACTAACCAATTCACCCCCCAACACCCCTCTACTGCTCATCTTTAAAAAATTAATAGTTT
CTATGGAAGCTACTAGATTAGAAATAATTTTCTTTTAATTTACTAGCAATTTTAATTCATGACTCTA
AGACTATAGAAAGAACTGTATGCGAGTGACAAAGTGTGACTAATTTAGTTTATTAATAAGACCTTGAAGAAAT
TGTGCAACTTAAGTGTATGACTGTGTGGCTGATTAATTTTGGCTTTTGAAGCTGGAAGCTGTGAGACATA
GAAATTTAATTTTCTTTCAGGACAGAGCTTGAAGAAAGCTATGAGAGTATCTAGTTAATCACTGCGACTAGT
GTGAAACCTTGGCTGGTGTATGTGATGGCTGTGGCTTTGAATGACTTATCATCTAGTCTTGTCTATTTT
TCTCTTGATGTTCAAGTCCGTAGTCTATAGGATGGCAATTTAAATGCTTTACTCCCCCTTTTAAAAATAATGAT
TAAATTTGCTTTTAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 38

MRPGLSFLALLFFFLGQAAGDLGDVGPPIPSPGFSSFFPGVDSSSSSFSSSSSRSGSSSSRSLGS
GGSVSQLFSNFTGSVDDRGTQCQSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALTKLKECEASKDQNTPVVHPPPTPGSCGH
GGVNVNISKPSVVQLNWRGFSYLYGAWGRDYSFQHPNKGLYWVAPLNTDGRLLLEYRYLYNTLD
DLLLLYNARELRITYGQSGGTAVYNNNMVNMVNTGNIARVNLTNTNTIAVTQTLFNAAAYNNR
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRMTNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSVLQKPQ



GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGTTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCCCATTTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCCATGGATGATTTCGTTATTGTATATAAATGCTCGAGAGTT
CGGGATCACCTATGGCCAAAGTAGTGGTACAGCAGTTTACAACAACATGTACGTCAACA
TGTAACAACCCGGGNATATTGCCAGAGTTTAACCTGACC

FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCCTTTGTGACGTTGTGGAGATGGGGGAGCGCTCGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGGAAGTGCCTGCTTTTGCTATGCCGATGCTGTGCTAGTGGGAAAC
 AACTCCCATGTAACTAGATTGATCTATGCACTTTTCTGCTTGTGAGTATGTGTAGTTG
 TGTAAATGTTGATACCAGGAATGGAAGAACACTGAATAGATTCTCGGATTTTGTGAGAAATG
 AGAAAGGTTGTTGCCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTCGCTAGTCTGCTATCTTCTCTCTTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAAATTA
 TTATTGGGCAATCTCTCATCTCCAGAAGGAACTTTACAACCTGTGTGGTTTATGTAGGCCATG
 GCAGGTGCCTTTTGTCTTCTCCATACACACTAGTCTTACTTATTGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAATGGAAAGGGGAACCTCGAGATGTGTGGTATGCAGCCTTGT
 TGTACGCTACAGCTCTGAATTAATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCATCCAGCAGTTCTCAGAAACAGGGCGTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT
 GTTACAGTCTTCAGTAATCAGTCTACACAATGTATTGACATGGTCAGCTATGACCAAT
 GAACCAGAAACAAATTTGCAACCCAGTCTACTAAGCATTAATTGGCTACAATACAAACAGCAC
 TGTCCAAAGGAAGGCGAGTCAGTCCAGTGGTGGCATGCTCAGGGAATTTATAGGACTAATTC
 TCTTTTGTGTGTTGATTTTATCCAGCATGCGTACTTCAAACAATAGTCAGGTTAATAA
 CTGACTCTAAACAGTATGAATCTACATTAATAGAAAGTGGTGGAGCTAGAAGTGTAGGATC
 ACTGGAGGATGGGACATGTTCAAGAGCTGTAGATAATGAAAGGATGGTGTGCACTTACA
 GTTATTGCTTCTTTCACCTTCTGCTTTTCCGGCTTCACTTTATATCATGATGACCCCTTACC
 AACTGGTCCAGGTATGAACCTCTCGGAGATGAAAAGTCAGTGGCAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTGATGTTTGGACACTCTGGGCACTTGTTC
 TTACAAATCGTGATTTTGACTGAGACTTCTAGCATGAAAGTCCCACTTTGATTATTTG
 TTTTGAACAGTATTCCAACTTTTGTAAAGTTGTGTATGTTTGTCTCCCATGTAAAC
 TTCTCCAGTGTTCGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAA
 TGTCATTCATATGTGAAGTGAATGAATTTGACAGAGGAAAGTTTATGAATATGGTGTAGT
 TAGTAAAGTTGGCCATTTTGGGCTATTTCTGCTCTATAGTTGTGAATGAAGATGAAAA
 ACAAATTTGTTTGACTATTTTAAATATATTAGACCTTAAGCTGTTTATAGCAAGCATTA
 GCAATGTATGGCTGCTTTTGAATATTTGATGTTGCTGGCAGGATACTGCCAAAGAAC
 ATGGTTTATTTTAAATTTTAAACAAAGTCACTTAAATGCCAGTGTGTGAAAAATCTTATA
 AGGTTTACCCTTGATACGGAATTTACACAGTATGGGAGTGTATTAGTGGCAATAGTGTAGG
 TTATGGATGGAGGTGTGCGTACTAAATTTGAATAACGAGTAAATTAICTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAAGTGTTTGCTTGTTTAACTCATGAAGTATGGGTTTCA
 GGAATGTTTGAAGCTCTGAAGGATTTAGACAAGGTTTGGCCAGCAGCGTAGCTCACCTT
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTTAGTTTGTGGCCAGCAGCGTAGCTCACCTT
 GGTAAATCCAGCATTTTGGGAGCTTAAGTGGGTAGATTACTGAGCCAGGAATTCAGCCCA
 GCTTGGCAGATGGTGAACCTGTCTATAAAATAATCTGCTTGTGAGCCAGGAATTCAGCCCA
 CAGCATGAGAGGCTAGTGAAGTGTGAGCCCAAGCCAAAGGTTGCAAGTGAAGTGAAGTGA
 CGTCACTGCACCTAGCTGGCAGAGTAAAGCAAAAAATATATATATTTGAATCAAGG
 AGGCCAAATTTTGACAGGGAAGGAAGTAACTGCCAAAAACCATAGGCTTTACTAGCTACTAT
 ATAAAACTAGTCCAGTTCTCTATTTAAAAAATGAACACATGAATACAGACTTAAATA
 GCTCAGATAGCTAATTAGGAATTTCAAGTTGGCCAAATAATAGCATTTCTCTGACATTTAA
 AATAATTTCTATTCAAATACATGCAATTTGATTACACCTCATAGTGTATTTAAATGTT
 GATGTGATTTGCTGGTGTCCAGCATGACCCATAAACAGTCAAGAAATGATGAATGTTT
 AGAATAAACTCTGCTTATAGTATACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTTGAATATATAGATTGTAACCTTCAACCTGAAATCAAGCAT
 ATGAGAGTTTAGTTTATTTGATGTGCTAGTGTCTAATGAAGCTTTTAAATCTACAAT
 TCTTCTTAAAAATTTTAAATGTGAATGGAATTAACAAATCAGTTTAAATTTCCCAACC
 TTATCTGTGTGTAGACATTTGATTCCACAATTTTGAATGGCTGTGTTTACCCTCTAAATAA
 ATGAATTCAGAGAAAAA

MGSVLGLCSMASWIPCLCGSAPCLLRCCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
 EQLNKIPGFCENEKGVPCNINLVGYKAVYRLCFGLAMFYLLSLLMIKVKSSDPRAAVHNG
 FWFFKFAAAIAIIIGAFPIPEGFTTWFVFGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
 EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYVYTHPASCSENKAFISVNMLLCVGASVMSI
 LPKIQESQPSRGLLQSSVITVYTMYLTSAMTNEPETNCNPSSLIIIGYNTTSTVPKEGQSV
 QWWHAQGIIGLILFLLCFVYSSIRTSNNSQVNKLTLTDESTLIEDGGARSDDGSLEDGDDVH
 RAVDNERDGVYTSYSFFHFMLFLASLYIMMTLTNWSRYEFSREMKSQWTAVVVKISSWSWIGI
 VLYVWTLVAPLVLTNRFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAACAANTCCACTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACCTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAACAANTCC
ACTGTAATTAGATTGATNTATGCACCTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC



FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCCTAGTGGAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACTTTTTCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTGTGAGAAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTGGTTGGC
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCGTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGGCGAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGCCGCGCGGCTCTCCAAT
 GGCATAATGTGTGGCTGGAGGGCAGCGCGAGGCTTTCCGCAAGCGCAGTCAAGTGTTCAGACAGCGGGCGAG
 TCCCTGTAAACGACAGATTAAAGAAACATTATTAACTGTCTATACGAGGGAGCGCCGCGGGGCTGTGCG
 ACTCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGARGAAGAAAGCGGAAAGCAGGAGATTCA
 GTCGTTTCCAGCCAAGTGACCTGATCGATGGCCCTCTGAATTTATCAGATATTTGATTTATAGCATGATCC
 CCCTGGTTTGTGTGTTACGCMACACACAGCTGCACACAAAGGCTCTGGCTCCCTCCCTCCCTGTTCCAGCTCC
 TGGGCGAATCCACATCTGTTCACCTCTCGCGGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTCGGAGTGT
 AAGAGGGACGAGGAAAGAAACAAAGCCACAGACGCACTTGAGACTCCCGCATCCCAAAAGAACACAGAT
 CAGCAAAAAAAGAAAGATGGGCCCCCGAGCCCTGTGTCTGTGCTGTCTGTCCGCACTGTGTTCCTCCCTGCTGG
 TGGAGCTCGGCTTCTGTGCGACACCGCTGAAAGGCGAGTTTCAGAGGGACCGCAGGAACATCCGCCCA
 ACATCATCTGTGTGTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCAGGTGATGAACAGACCCGCGC
 ATCATGGAGCAGGGCGGGCGCACTTCATCAACGCTTCTGTGACCAACCCATGTGTGTCCTCACGCTCCTC
 CATCTCTCACTGGCAAGTACGTCCAACACACACCTACACCAACAATGAGAACTGTCTCCGCTCCTGGC
 AGGCACGACGAGAGCGCACCTTTGCCGTGTACTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG
 TATCTTAATGAATACAAACGGCTCCTACGTGCCACCCGGCTGGAAGGAGTGGGTCCGACTCTTAAAAACTCCCG
 CTTTATAACTACACGCTGTGTGCGAAGGGGTGAAAGAGAAGCAGGCTCCGACTACTCCAAGCTTACCTCA
 CAGACCTCATCAGCAATGACAGCTGAGCTTCTTCGCGAGTCCAGAAAGATATCCCGCAGCAGGCCAGCTCCT
 ATGGTCATCAGCACTGACGCCCCCAGCGGCTGAGGATTCCAGCCCCATATTCAGCCTCTTCCCAAAAGC
 ATCTCAGCACTCAGCGGAGCTACAACTACGCGCCCAACCGGACAAACATGGATCATCGGCTACAGCGGGC
 CCATAGGCCCATTCACATGCGAATTACCAACATGTCTCCAGGAGCGCTTGCAGACCTCATGTCTGGTGGAC
 GACTCCATGGAGACGATTTACACATGTCTGGTTGAGACGGGCGAGCTGGACAAACATGTACATGTATACACCGC
 CGACACGGTTTACCACATCGCCAGTTTGGCTGGTGAAGGGAATCATGTCCGATGAGTTTGCATCAGGG
 TCCGCTTCTACGTGAGGGGCCCAACGTGGAAGCGGCTGTCTGTAATCCCAACATGTCTCAACATTGACCTG
 GGCCACCATTCTGGACATTTCAGGCTGGACATACCTGCGGATGCGAGGGAATCCATCCTCAAGCTG
 GGACCGGAGCGGCGCTGATGATCGTTTCACTTGAAGAAAGAGATGAGGCTGTGGCGGACATCTCTTGTGTG
 AGAGAGCCAGCTGCTACACAGAGACAAATGCAAGGTGGAGGCCACGAGGACCACTTCTGCCAAGTAC
 CAGCGTGTGAAGACCTGTGTACGCTGTGAGTACCAACGCGCTGTGAGCAGCTGGGACAGAAGTGGCAGT
 TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAGAGGCCCATCGGCTGGGCGGACGACAGCC
 TCTCAACCTCTGTGCCAAGTACTACGCGCAGGGCAGCGAGGCTGCACTGTGACACCGGGCTACAGACTC
 AGCCTGCGCGGACGCCGAAAAACTCTTCAAGAGAAATACAGGCCAGCTATGTCCGAGCTCGCTCCATCCG
 CTCAGTGGCCATCGAGGTGGACGGCAGGCTGTACACGTAGGCTGGGTGATGCGCGCCAGCCCGAAACCTCA
 CCAAGCGGCATCGGCGAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGAGCTTCAGTGGCACTGGAGG
 CTTTCCGACTACTCAGCGGCCAACCCCTTAAAGTGACACATCGGTGCTACATCTTAGAGAACGACACAGTCCA
 GTGTGACCTGGACCTGTACAGTCCCTGCAGGCTGGAAAGACCAAGCTGCACATCGACACAGAGATTGAA
 CCTCGACAAACAAATTAAGAACTGAGGGAAGTCCGAGGTCACTGAAGAAAAGCGGCCAGAGAATGTGAC
 TGTCAACAAATCAGCTACCAACACCGAGCAAGGCGCGCTCAAGCACAGGGCTCCAGTCTGCATCCTTTCAG
 GAAGGCTGCAAGAGAAAGCAAGGTGGCTGTTCGGGAGCAAGGCGCAAGAAACCTCCGAAAGCTGC
 TCAAGCGCTCGAGAACAACGACAGCTGCAGCATGCCAGGCTCAGCTGTCTACCCACGACACACGAGCATG
 CAGACGGCGGCTTCTGACACTGGGGCTTCTGTGCTGTGACACGCGCAACATTAACAGTACTGTGTGAT
 GAGGACCATCAATGAGACTCAATTTCTCTCTGTGAATTTGCACTGGCTTCTAGAGTACTTTGATCTCA
 ACACAGACCCCTCAGCTGATGAATGCAATGAGACACTGGACAGGATGTCTCAACCACTACACCTACAG
 CTCATGGAGCTGAGGAGTGAAGGTTTCAAGGAGTGAACCCCGGACTGGAACATGGACCTGGATGGAG
 AAGCTATGACCAATACAGGCACTTTCAGCTGCAAGTGGCCAGAAATGAAGAGACCTTCTTCAACATCTGG
 GACAACTTGGGAAGGCTGGGAAGGTAAAGAAACACAGAGGTGGACCTCCAAACATAGAGGCATCACTGA
 CTGACAGGCAATGAAGAACCATGTGGGTGATTTCAGCAGACCTGTGCTTGGCCAGGAGGCTGAGAAAGC
 AAGCAGCAGCTCTCAGTCAACATGACAGATTCTGGAGGATAACCCAGGAGCAGAGATACTCAGGAATCC
 ATTTTTCCTGCTTGTGTTGTTGATTTATACCTACCAAGTGCACAAATGCAATTTTCTGATCAAAAGTC
 ACCACTAACCTCCCGAAGCTCACAAGGAAAGCGAGAGAGCGAGCAGGAGAGATTTCTTGGAAATTTTC
 TCCCAAGGGGAAAGTCAATGGAATTTTAAATCATAGGGGAAAGCAGTCTGTGTTCTTAATCTCTTATTTCT
 TTGTTTGTGCACAAAGGAACTAAAGAGCAGGACAGAGGCAAGCTGGAGAGGCTGAAACACAGTCGAGAGC
 TTTGACATGAGTCAGTAAAGCAAAAGAGATGACATTTACCTAGCACTATAAACCTGGTTCCTCTGAAGAA
 CTGCGCTCATGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTAGGGGAACCTAATAAGAAAT
 CCAATTTTCAGAGTGGTGGTGTCAATAACGCTCTGTGCCAGTGTAAAGAAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIIILVLTDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTPMCCPSRSSIITGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPEYFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAAQEE
FLPKYQVRKDLQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYK
LQAWKDKHLHDHEIETLQNKIKNLREVGRHLKKRPEECDCHKISYHTQHKGRLKHRGSSL
HPFRKGLQEKKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCACTSANNNTYWCRTINETHNFLCFEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCGKYQCNPRTNRMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCAGATGCTGGGCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGGCCACC
TGCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGAAA
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTACAC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCAGCCACCATCCCCGCCA
CGCTCGCTGAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGTACTATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTCGGGGCTGGACAGCCGCTTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTCATCGGTGCCTTAGTCCAAGAAAAT
AAAAACCCTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 49

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFRR
 RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRRHPRHAR

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FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTAGGGCTACTGGCTGGGTGGAAGTGAGTGCTGGGTACCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC
 TGCAGCATCTCTCCGAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCTTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAAGCTTGAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGTGCCACACTGTACCTGGGGCAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCTCCTTCTCTGGGGAGGAGGGGTTCTTGAGGGACCTGACTTCCCTTGC
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGCTTTTTTTCAGACTC
 ACAGTGAGGACTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAA
 AAAAAAAA

MSDLLLLGLIGGLTLLLLLLTLFAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRVRHPALDITYKERKLCAYPRLEIYQEDQIHMCPLAR
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSAATLSPGAS
SRGWDGDGTRSEHSYSSESAGSGSSFELDLEGEGLGESRLDPGTEPLGTTKWLEWPTAPEK
GKE

FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
GCCCCGCGCCAGT**CATG**ACCCTGCGCCCCCTACTCCTCCCGCTCCATCTGCTGCTGCTGCT
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGA
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
GATTGCTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
AGACCCAAAGTCTCCAAAAAGAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
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FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGAGAGCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAGGG
ATGGCCATGGTGCCACCCCTCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCCGTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGAAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTTAAAAAACTTAAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCTGGATTCTAGAGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTATATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACACCTAAACAACAACCAAAATCTATTGTGGTATGCACCTTGATTAACTT
 ATAAAAATGTTAGAGGAACTTTTACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAAT
 GTAACCTGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCAGT

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
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DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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FIGURE 58

TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTCAACCANTCATACC
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTCCAGAATGCCTTC
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTTCCAGAATGCC



FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTGCGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAGACATAG
TATACCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

[illegible]

FIGURE 64

MWLPLVLLAVLLAVLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGSSEIAFHTIPVIQRA
GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPFGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYVVYDMDQAMERYVSMFREEAAEH
IPLLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

[illegible]

FIGURE 66

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLSKTTTLTSDESVKDHTTAGRVVAGQIFLD
 SEESELESSIQEEDSLKSQEGESVTEDISFLESPNPENKDYEPPKKVRKPALTAIEGTAHG
 EPCHFPPFLFLDKEYDECTSDGREDEGRLWCATTYDYKADEKWGFCETEEEAARRQMGEAEMM
 YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEX
 LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLIAMVVLVSRL

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTACCATCAGGGACTACGGTGTGTCCTGG
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCCTCCCCTCTGCCTCCCATTTCT
GCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVPEDDADYICSVGYGFSP



FIGURE 69

GCGGCCCGCCCCGAGACCGGGCCCCGGGGCGCGGGCGGGCGGGATGCGGCCCGCGGGCGG
 CGATGACCGCGGAGCGCAGCGCCGCGGGCCCCGGCCCTGACCCCGCGCGCGCGCCGCTGAGCCCC
 CCCGCCGAGGTCCGGACAGGCGCGAGATGACGACCGCGAGCCCTGTTGCTGCTCTGCTGCCC
 CGCTGCTGCTGGGGGCGCTTCCCACCGCGCGCGCGCGCCGCGGAGCCGCCCAAAGTATGCCGCG
 AAGGTGGTCCACGCGCAGGTGGCCCGGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GGGGGACCGCGCGCGCTGACCATGTGGACCAAGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GCGCGCTTCCGCGCTGCTGGCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGCG
 GTGTACGTGTGCAAGGCCACCAACGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GCTGGATGACATTAGCCAGGGGAAGGAGAGCTGGGGCCCGCAGCGCTCTCTGGGGGTCAGG
 AGGACCCCGCGCAGCGCAGCTGGGCGACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGG
 CGGGTGATCGCACGCGCCCTGGGTAGCTCCGTGCGGCTCAAGTGGCTGGCCAGCGGGGACCCC
 TCGGCCCGACATACGTGGATGAAGGACGACAGGCGCTTGAACGCGCCAGAGGCGCGCTGAGC
 CCAGGAAGAAGAAGTGGACACGTAGGCTGAAGAACCTGCGGCGCGGAGGACAGCGGCAATAC
 ACCTGCCCGCTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAGGCTGGATGTGATCCCA
 GCGGACCGCTTCCAGCGCGCTGCTCAGCGGCGCGCACCCCGTGAACACGACGCGGTGGATCTCG
 GGGGGACCGCTCTTCCAGTGAAGGTGCGCAGCGTGAAGCGGGTGAATCCAGTGGCTG
 AAGCGCGTGGAGTACGGCGCGAGGGCGCGCGCAACTCCACCATCGATGTGGGGCGGCCAGAA
 GTTTGTGTGCTGCCACGGGTGACGTGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 TGCTCATACCCGTCGCCCGCCAGGATGCGGGCATGTACATCTGCTTGGCGCCACACAC
 ACTGGCTACAGCTTCCGCGCGCGCTTCTCAGCTGCTGCCAGACCAAACCGCGCGGCG
 ACCTGTGCGCTTCTCGCTCGGCCACTAGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 CGGCGCTGTCTTATCTTGGGACCGCTGCTTCTTGGCTTTGCCAGCGCGAGGAAGCG
 TGCACCGCGCGCGCTTGGCGCTTCCCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 GCGGGAGACAAAGACCTTCCCTCGTTGGCGCGCGCTCAGCGCTGGCGCTTGGTGTGGGGCTGT
 GTAGGAGCATGGGTCTCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 CCTAAGTTGTACCCCAAATCTACACAGACATCCACACACACACACACACACATCTCACAC
 ACACCTCACAGCTGGAGGGGCAAGGTCCACGACACATCCACTATCAGTGC**TAG**ACGGCACCGGT
 ATCTGCACTGGGCGCGGGCG
 CGCAGCAGAGGCGAGGGGACCCATGGCGAGGACACACACAGCATGCCAGCACCGCAGCGCTGTGTG
 TGAGGCATAGCCCTGGACACACACACACACAGCAGCATACCTGGATGCTATGATATCAC
 ACACATGCGCGCACAGCTGCTCGCTGAAGGCACAGTACGACACACACACACACAGATATCG
 CGCGCTGGGACACAGATAAGCTGCCCAAATGCACGACACACGACACAGAGATGCCGAACA
 TACAAGGACATGCTGCTGAACATACACACGACACACCATGCCAGATGTGCTGCTGGACA
 CACACACACACACAGGATATGCTGTCTGGACGACACACAGTGCAGATATGCTATCCGGACACA
 CAGTGCACAGATATGCTGCCCTGGACACACATCCAGCAGACAGTGCACAGCGCAGATATGCT
 GCCTGGACACACAGCAGATATGCTGTCTAGTACACACACACGCGAGACATGCTGTCCGACAC
 ACACACGATGCACAGATATGCTGTCCGGACACACACACGCGCAGATATGCTGCTGGAC
 ACACACACAGATAATGCTGCCTCAACACTCACACACAGTGCAGATATGCTGCTGGACACACACA
 TGTGCACAGATATGCTGTGGACATGCACACACAGTGCAGATATGCTGTCCGGATACACAGC
 CAGCACACATGCGAGATATGCTGCCTGGGACACACTTCCGGACACACATGCACACACAGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCCTCAACACTCACACAGTGCAGATA
 TATTGCTGTGGACACACATATGTCACAGATATGCTGTGCGACATGCACACAGTGCAGATA
 TGTGTGTCCGGATACACGACGACACACATGCAGATATGCTGCTGGGACACACTTCCGGAC
 CACACATGCACACAGGTGCAGATATGCTGCCTGGACACAGCAGATGACGTGAGCTTTTGG
 GAGGGTGTGCGGTGAAGCGCTGCAGTACGTGTGCGGTGAGGCTCATAGTTGATGAGGACTTT
 CCCTGCTCCACCGTCACTCCCCAACTCTGCCCCGCTCTGTCCCCGCTCACTCCCCGCTCT
 CATGCGCGCTGTGCTCCCTGGCTTGGCGGCTATTTTGCACCTGCTTGGGTGCCAGG
 AGTCCCCCTACTGCTGTGGGCTGGGGTTGGGGGCGACAGCCCCAGGCTGAGAGGCTGGAG
 CCCATGGCTAGTGGCTCATCCCACTGCATTCTCCCCCTGACACAGAGAGGGGCTTGGTA
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTGCAGGAC
 TGTGGTCTCTCTGGGCGCGCGGACCGCGCTGGTCTTTCAGCCACTGCTGATGAGGACCCG
 GTCCAGGCGACACACACCCCCACCCCACTGTGCTGGTGGGCGCGAGATCTCTGTAATTTTA
 TGTAGAGTTTGAAGCGCCGATATTTAATTTATTTTGTAAACAAAA

MTPSPLLLLLLPPLLLGAFPPAAAARGPPKMA DKVVPQVQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK
ESLGPDDSSGGQEDPASQQWARPRFTQPSKMRRRVIA R PVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV L
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGHRNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTL L L WLCQAQKPKCTPAPAPPLPGHRPPGTARDRSGDKDLPS
LAALSAGPVGVLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHSHSHVEGKV
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FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAATCTCCAGGGGACCAGCATTCCAGAGTCT
 AGTGACTCTCTGGAAGACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAACATGGTGGGGACCA
 AGGCGTGGGTGTTCTCTCTCTGCTGGTCTGGAAGTACATCTGTGTTGGGGAGACAGCAGATGCTCACCCAGTCA
 GTAAGAGAGTCTCCAGCTTGGGAAGAAGAACCCAGCATCTTGGCCAGGCTGCCGACACCTTGAGAGCCCTGG
 TGAGTGGACACATGCTTCAACATCTGACTACCCAGGGGGAGGGCGACTATGAGGGCGTGGAGCCCTTCCGCT
 TCTACTATGGGACAGCTGTATGCTCCGCTCCCTGCGCTGAGGCTCGGACACTGACTGTGACACCTTGGGGC
 AGCATTGGCCAGCTGTCTGCTGACTCCCTGAGGCTTTCTGGCTGCTCAGGAGTCAAGCTGAGCTGAGCTGGA
 GAACGTCTTAATTACACCGTAGCTCTCTCTGCGCCACAGGATCCCTGCGCGACACAGACAGCCATCTGGG
 GCCCATGGTCTCCTGGAGCAAGTGCTCAGCTGCTCTGGTCAAGTGGGCTCCAGACTTCGCACACGATTTGCT
 TTGGCAGAGATGTTGCTCGCTGTGCAGTGAGGCCAGCGAAGAGGTTCAAGTGCATGCTGGGCGAGGACTGTACAGC
 CTGTGACCTGACCTGCCCAATGGGCGAGGTGAATGTGACTGTGATGCTGCTGAGTGGCCAGGACTCTCATGTCTTC
 ATGGGCTGTGCTCTCTCTCCGAGGCTGCCAGGCTCAGGGCTGCTATCTGACTCTGACCCAGAGCGCCGAG
 CTGCTGACCCAGACAGACAGCTGAGGGAGATTCCGATCCCTGGCTGTATGCGCAAAAGCATCTTGA
 GATCACAAGGTCAAGTTTGGCCCATTTGATCTACAATGCCAAGACTAGCTTGAAGCGAGCCACCATCAAG
 CAGAGTTTGTGGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAGCAGGAGAGCTGGGCAAGC
 GTGTCTCTGTGCTGTAAAGGCCACAGGGAAGGCCAGGCCAGACAAGTATTTTGGTATCATATGATGACACATTTGCT
 GGATCTCTCCCTCTACAAGCATGAGAGCAAGCTGGTGTGAGGAACCTGCAGCAGCCAGCCAGCTGGGGAGTACT
 TTTGCAAGGCCAGAGTGTATGCTGGGCTGTGAAGTCAAGTTGCTCCAGCTGATTTGACAGCATCTGTAGTG
 ACTCTCTGCAACCTGACTCTCCGAGAGCTATCTATCCGCTGCCCTTGTGCTTTCAGAACTGCCCACTCTG
 CTTCTACTATCAGCTGGGACGCTGCCCTGTTAAGACTTTGTGCAGGCGAGCAGGATAATGGGATCAGGTGCCGTG
 ATGCTGTGCAGAGCTGCTGTGGCATCTCCAGACAGAGGAAGGGAGATCCAGTGGCTGGGTCACAGCTACCC
 ACCAAGGTGGCAAGAGGTGACCTGCCAGCGGTTGACGGAACCTCGGAGCATCTGCTGGGGGCCGCTGTGCTG
 TGTGACAAATGGGGAGCCCATCGCTTTGGCCATGTGTACATGGGGAACAGCCGCTGTAAAGCATGATGGCTTACA
 AGGCGACTTTCCACTCATCTGCCAGGACCTGAGAGGCTGGTCTCACAATTTGTGGACAGGCTGCAGAG
 TTTGTCAACACCAACAAAGTGTACTCTTTCAACAAGAGGGGAGTGGCTGTTTCATGAATCAAGTCTGAG
 TCGGAAGAGGCCCATCACTTTGAAGCCATGGAGACCAACATCATCCCTCGGGGGCAAGTGGTTGGTGAAGACC
 CCATGGCTGAATGGAGTTCCATCCAGGATTTCTACAGGCAAGATGGGGAGCCCTCATGTAGGAAGAAATGAAG
 GCCAGTGTGACCTTCTCGGATCCCGGAATATTTCCACAGGCCACAGCTGCCAGACTGACCTGAACCTTATCAAA
 TGACAGAGGAGACATTTCCCTTTCCGAGCATGTGGCATTTCTCTGTGGACTTCAGAGATGAGGTCACCTCAG
 AGCCCTTATGCTGCGAAATGAAGTCCACTTTGATCTGACCCAGGCTCAAGATGCGCAGAGCACATATCAACA
 GTGAACCTTGTGGTCACTCAATCCAGACACAGGCGTGTGGGAGGAGGAGTGTATTCATATCAAAATCAAG
 GAGGAACAAAGAGAGACAGCAACCTTCTGGTGGGCACTGGAGTTCTGTGAGAGGAGCTCTTAACCTGG
 ATGTTCTCGAAGCAGGCGGTGCTTTGTTAAGGTGAGGGCTTACCGGAGTGAGAGGTCTTGTGCTAGTGAGCAG
 ATCCAGGSGATGTGATCTCGTGATTAACTCGGAGCTAGAACTGGCTCTTGTGCCAACCTAGGGCCGTGGGG
 CGCTTTTGAAGGCTGTATCTGACAGGCCCAACGGGCTGTGCTGCTGCTCTGCTGTGATGACAGCTCCCTGATG
 CTTACTCTGCTCATTTCTTGCAGGCTGCTGCTGGGAGGAACTGCAAGCATGAGCTTCTCTCAATTAAC
 CCAAAATGCAATTGGGCTCCTTCAGCCCTATCTCAACAAAGCTCAACTCCGTCGGAGGCACATGAGGATCCAG
 GGTAAAAAGACAGCTTTCCAGATTAGCATGGCCAAAGCCCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGGCCA
 TCTATGCTTTGAGAACCTCCGGGCATGTGAAGAGGCCACCCAGTGCAGGCCACTCCGGTCTTACCAAGATT
 ATCCAGGSGATCGATTGACTACACACAGTCCCCCTCAACGAAGTAGCCCTATGAGCTGGACTGAAGACTATCT
 GCAATGTGGCCAAAGCCGTGAATTCAAGGCTCTATATCAAGTGAAGATGTGTGGGCGACTGGAGGTGA
 AATGGCGATCCCGCAACATGGGGGCACTCATCGCGGCACTGGGGAGCTGTATGATGATCCAGTGTGAGG
 AGCATCTGGGACAGGAGCAGCCCAATGTCTCAGCTGCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA
 TCAAGCAGCTGTGGGACCGCACCTTGGTGAAGTCTATCCCGAGGSCAGCTGCCCTGACGCCAGTGTGAACCCA
 TGCTGCATGAGTACCTGTGTCACCACTTGCCACTTGACGTCAACAGCAGCAGCTGAGTACACCATCTGGCGA
 CCTTGGGACCTGGGCACTGGGCACTTGGCTCTTCACTGTCACTGACAGCCAGCCCTGCAGCGCCCAAGAGAT
 CGCGCTCGGGGGCTTTGATGCGACATCGATGGCTCTCCAGATCATGAAGCATGAAGGACATGAAGTACCT
 TCAACTCTCACTGTGTGAGAGGCAAGTAGGCGCGCAGAGTGCTTCCAGTACCTCTCAAGACACCCCGCCAG
 TCCCTCTGCTGAGGCACTGTCAAGGAAGAGTGCCTCTGAGGAGGCGCAGCAGGAGCGAGGCTGGCGAGCG
 CCAGGTTGGGCTGGTGGCTCTCTGAGATTCTCTAGAGTTGCTCAACAGCCCTCTGATCAACTAAGTTTGTGGT
 ACTTCCAGCTCTTCTGCGCCATTTCTCATGTGACAGCATTTGTGAGACTGTGACAAACATGTCACTTGGTTAAT
 TTAAGCACTTCTCTGCAATTGCTGTGTTGTTCTCATGCTCTTACTTACTTTGTCGCTGACTCTGA
 TTGGCAGTGGGCCCCCAATGGCAATTAAGCCCTTGTGAACTCTGCTTCAATTAAGCAAAATATCTTCTCTTCT
 GGCCATGTGTAATACTCTGCACTTCAACTGTACTTCAATTAAGTCAAAATATCTTCTCTTCTTCT
 TTTTGCATGGTTTGGCCACTCTGCAATAGTGATAATCTGTATGCTGAAGATCAATAACCAATATAAGACATAT
 TTTTGGCCTTGTCTGCCAGGACATAGGCAAGCCTTGATCATAGTTTATACATATAAATGGTGGTGAATAAG
 AATAAACAACATATCTTACTTGAAGTGAATAAATATTTATTTCTTGTCTAAATTTGGAATTTCTAGTGC
 ACATTCAAAGTTAAGCTTAATATAGGGTACATAGTTCTCTTCAAGCTGCGGAAGACATCTCCCTGGT
 ATCCAAATTCACAGTTTCACTTAACTCCCTTCACTTCTCTTTGTTCTTCTGTAAGAAC
 CCAAGTGTAGCCAGGCGAGATGTCAATAAATGCATACTCTGTATTTTGGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI
 DYPGGKGDYERLDAIRFYYGDRVCARPLRLARTTDWTFAGSTGQVVHGSPEGFWCLNREQ
 RPPGQNCSTYTVRFLCPPGSLRRDTERIWSWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPCLLTQTDSGRFRIPGLCPDGKSLKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCKATGKPRPDYFWYHNDTLLDPSLYKHESKLVLRLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQATNSFYDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCKISKTEEREIQCSGYTLPTKVAKECSCQRCETRSIVRGRV
 SAADNGEPMRFGHVIMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELIPSRSFYRQNGEPYIGKV
 KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRNRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRTDHEDPR
 VKKTAQFQISMAKPRPNSSAESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTPPFN
 EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRVTGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPOGSCRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMPLAPLDPLGHNYGIYVTVDQDPRTAKEIALGRCFDGTSBGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCCATAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTCATATTTGGTTTGGGATCTGCTTTGAGGTCCTCATTTAAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATACATATCTGTATATATATCTAAACTAGACAAAAGATCCGACATCATTAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAAGAAATTTAGAGAGCTATTTGTCAAGATCCCTGTCGATTCATG
 CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCTTTGGTTTGGGGACATTTATGATTTTGTGTAAGACT
 CAGATTTACACGGAAGAAGGGAAGTTTGGGATTACATGGCTGCCAGCCGGATCCACGGACATGACAAAATA
 CTGTAAAGTGAAGCTCGATCTCCGGATATTACCTGTGGAGACCCCTCTGAGACGTTCTGTGCAATGGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGTATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCCTTGGGAAGGATATCCCAAGCCCTCCAGGTTAACT
 CACTCTGCTTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGGCGTCCAGACC
 AAATGATCCTGGGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATACAGCATACGGTCTTAGAAATCATTTGCACAGA
 AGAGTACTCAACAGGGTATACAACAATAGCAAAATATCCACTTTGAATCAAGACAGGTTCCGCGCTTTTG
 CTGGACCTCGCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACACCAAGAACTCAGAGATTTCTT
 ACAGTACAGACTGAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAAACAGCAAAATTCAGATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGA
 AATTATCAGGGCCGACTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGTTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCCCCGGCGCATACACGGGCATCTCTGCGAGAAGCTCGGCTGCGAGGAGCTGGC
 AGCTCGCGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCAGGCGTGTGCTGCTGACACAGCTGTCT
 GGGAAACCGCAGCCCCCTGGTGTCTAGGTGTCACTCCAGCCACACGGGACGGGCTGTGCGCTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTTAACATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCAATCCCGAGTCAAGACTGTTATTTCT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAATACATTTGCCAGCTCCAGAGCATTTTGTGGA
 TTGGAAAGGCTGGCAGCCCCCCCCAACAGGAAGACAAAACAACAAATCAACCGACTCAAAACAAATTGGC
 TACTCTAGCTGTTGGCGCCCTPAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCAATTTCTTGTCTGAG
 GTGCAATTGTGGGCATAAGGAATCTGTTACAGCTGCCATATTTGSCCTGCTCCGCTCCCTGAATCCCTCCAC
 CTGTGCTTTAGTGAACGTGCTCTGTAAACCTCTGTTGTTTGAAGATTTCTTTGTCTGATTTAGTGAAGCA
 TGTGTAAACAGCCCCCTCTAAAGCGCAAGCCAGTCAATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCCACTATAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCCCTTTGTATTCAAAATGAAGTT
 ATTTTCTTGAACACTCTAAATGTAGATTTTGTATTTATTTGCCAATTTGTGTTCCAGACAATCTGTATAT
 GTATCTAATTCGAATCAGCAAGACTGACATTTTATTTTGTCTCTTTCTGTTCTGTTTGTGTTCTACTGTGCA
 GATTTCTCTGTAGGGCAACGAACGTGCTGGCATCAAGAAATATCAGTTTACATATATAACAGGTGAATAAGA
 TTCCACCAAAAGGCATTTCTAAATGTGTTTCTTGTGCTTTAACACTGGAAGATTAAAGAAATAAAAACTCTGCA
 TAAACGATTTCAAGAAATTTGATTTGCAATTTCTTAAGATGAAAGGAACGCCACCAAGCAGTTTTCACACTCACT
 TACTGATTTCTGTGTGAGCTGAGTACATTCAGCTGACGAATTTAGTTTCCAGGAAGATGGATGATGTTTCACT
 AGCTTGGACAACTTTTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAA

MYLSRSLSIHALWVTSSVMQPYPLVWGHYDLCKTQIYTEEGKVDYMACQPESTDMTKYLK
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYPKPLQVNIITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDL SQHTVLEI ICTEEYSTGYTTSKIIHFEIKDRFALFAGPRLRNMA SLYGQLD
TTKKLRDFFTVDLRI RLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKNLHATVCVYDN
SKLTCECEHNTTGPDCGKCKNYQGRPWSPGSYLP I PKGTANTCIPSISSIGTNVCDNELLH
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQAGPHGTPALLLLTTLGTAS
PLNG

FIGURE 75

CCCACGCGTCGGGTGACCTGGGCCGAGCCCTCCCGGTCGGCTAAGATTGCTGAGGAGGCGG
 CGGGTAGCTGGCAGGCGCCGACTCCGAAGGCCGCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTTGGACCA**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCCAAGATTTTTTGGAAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGCTGGCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTCCGGGACGTGGCCTGCATGGCTATCTGCTCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGAGACCCGTGGTGGGAATTCACAGCTTCTCATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTTCTTGAGTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACCCGATGCACTTGGAGCCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTCGAGGAGTTCACCTTGCAGAACATTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGAAATCTCATCAGCAGGAGCCTGTGGA
 AAAGGGCATGTCAAGTAACTCTGGGAATGGCTGGATTTCGGAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTGCCACAAGCGCCTTTTATTTAGGGTAAAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCTTACATTTATATGATTCTGGGGTT
 GCTTCAGAAGTGTTATTTTATGAATCATTATGATTTGATCCCCAGGATTTCTATTTTGT
 TTAATGGCCTTTTCTACTAAAAGCATAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT
 TTACTTTACATATTTCGTTTTTCAATACTTGCTGTCTCATGTTACACAACTCAGTAGTACAACC
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC
 TAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFFACVVVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
 SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVW
 HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
 LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 77

TGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAG
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCTGAGCGAGCCTAGTGGCGGGTGTTTGCATTGAACAGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCGTCCCTTTAAAGGGCGGGCGTCCGAGCAGCTGTATCTGAGCCCGAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGCGGGGCTT
 CCTCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCACTCATGCTGAGCAGAGTA
TGGAAGCACCCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCACACTGTACATCCTCTGCCACATCTTCTCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCTGCTCGGAACACTACTACATCCAGTGGCT
 CAACGGCTCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAG
 GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGATCTCTCTTCTCTGGGTTCTG
 CTGCTCCTGTGTGTACTCCACTGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGCGGAAGGC
 TTCAGCTTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGGTGTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTCACTCAGGTGTGACTCATCTTTTACCTAATGGTGCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGACACTGCCATGACGCAGATAATT
 GGGAACTGTGTCTCTCTGGTCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGACGGCTCACCACACTGTCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCGT
 CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGTGGGA
 AGGAAAACTGGACACTGCCATCTGCTGCTAGGCCCTGGAGGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGAACTGGAACTCTGAGAGGGTGGGTGGCAGAGGGGAGCAGGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCTGCTTTTCCATACTTAACTGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCGATCCCAAATCTGTTTACACATCA
 ATCTGCTCACTGCTGTCTTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT
 AGGGTGGGGTAGGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCTCTGGCCGAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTACGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVL SVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATV NK
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIIQWLNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGV LGRVYETVVM LMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMF SVTGKLLVKPRLLLEDLEEQLYCSAFEE
AALTRRICNPTSCWLP LDMEL LHRQVLALQTQRV LLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMP RGMQGTSLGQVSF SKLGSFGAVIQVVLIFYLMVSSVVG FY
SSPLFRSLRPRWHD TMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLG NFY
IVFLYNAAFAGLTTLC LVKTF TA AVRAELIRAFGLDRLPLPVSGFPQASRKTQH Q

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTG
CTGCCCCTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC**ATG**CTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTGAGTGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG
GCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCCTGGCATTCCCTTAATAAAAGAACTGACTTCAAAAAAAAAAAAAAAAAAAAA
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FIGURE 83

MLLWVILLV LAPVSGQFARTPRPIIFLQPPWTTVFQGERVTILTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSSDLLT

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FIGURE 84

CAGAAAGAGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGCCTCACAGGGCCGGGTGGCTGGCGAGCCGACGCGGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACATGGCTCCGAGAACCTGAGCACCTTTT
 GCCTGTTGCTGCTATACCTCATCGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAGGAGGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCTGTGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGAAGAGAT
 GCGGACCAACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAGTGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTATTTGGAGAAGGTGAGCCTCACGTGGATGGGAGCCTGG
 AGATTTACGGTCCGAATCAAAGTTGTCAAGCACCAATATTTGAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAACTCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAGAAGTTAACAGAGGAAGCGAGAGAAGGTATCAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAATGCCAAGTGGAGAAGTCTGTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDDPQ
 AQEKFQDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTFRQQ
 DRNIPRGSIIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
 MTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMIEYPFIGEGEPHVDGEPGDLRFRIKVVKH
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAAGGGAACCCGGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGCGGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACTGAGCAGNTTTTGCCGTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTTAAAAGG
CCTATAGGAAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCGAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGGTGAAGAAGGATTAAGAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCGCTTNGTCAGCAAGACAGA
AATATCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGCGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTCTGGCTTCGTTTGACGCC
 TTGGTGTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC
 AGAGAAGCTTGTGGCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC
 TCACCTGGTGTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCCAGGCCCTGAAGGCTTCTGACAGGAGCAGTCTGCAATTT**TAGT**GCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTTGCCGCCATCCCTGGATGGCTCAGCTTAGCCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAAGTTCGAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTCACATTAAATTTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGAAGACTTGACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAAC
 ACAAAGTTGATGATTTCTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTGCGCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTCAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTTCTAG
 GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACATATGGTATAACAACA
 AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAATACATGAAATAGCTTGAATGTTCTTTACAGGAGTTTAAACCGTATAG
 CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCCTGTTTCTTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGCCACTGCAATGGCAAAAATATTTCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
 ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFQK
 HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGI
 RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
 ACCNTGGGCTTTCGGAGGTGCTTCGCCGCTGTCCCACCACTGCAGCCATGATCTCCTTAA
 CGGACACGCAGAAAATTGGAATGGGATTAAACCGGATTTGGAGTGTTTTCTCTGTTCTTTGGA
 ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTGTAGCCGGCTT
 GGCTTTTGTAAATTGGTTTAGAAAAGAACATTTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
 CTACAGGTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
 ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGTGCCAGGAAGGAGACGCCCTTCCTGAGTCTCGATCTTTCTTCCTTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
ATCAACACCATTAGCTCTTCACTCTCCTCCTCTGGCCCCATTAAACAGCAGCTCTTCCGGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
ACGCTTTGGGCTGTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTCGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTCTCT
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTAGAAA
TAATGAAAATCCAACACTGCTGGGAGTCTTAAACGGAAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCAGA
GACGCCCATGGTGCCCCCGGGGGCCCTGGACCCTCGTGAAGTGGCTGTTTTGGGCCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCTTGGTGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCCTCGTCTTCTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGAGGTGTCAACATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACCTTTGTTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAGTTCCCTTTTCATCCTTTGGTGCTGAGTTTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIAAGLIINTIQLFTLLLPINKQLFRKINCRLSYCISSQLV
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFATVRSRLRNVS AVYDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRWMIGVTEIDKGSAYGNSDS
KQKLND



FIGURE 94

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTCTTCTTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTGAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCCTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCCGTCGTATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTTGACAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGTCGTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAAACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGAACATTTTCTTTGTGTCAGGCATTA
 CGGACCTTTTTCCAAATTCGAAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACACAACCACCATCTCGATGTAGTAGACAAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC
 CAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTACGGTCTCCTACA
 TTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCACAACTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCAGCACCTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCACGTTATTGAGACCATGTCTATTAATAAATAAATGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAAATTCCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAATAAAAAAAAAAAAAAAAAA

MEGESTSAVLSGFVLGALAFQHLNTSDSTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTSPSIITESCSTHRLHSLYKPKQGLFHRVPLVVANLGMSEQLGKTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPQENIFLCQALRFTFFPNEFLHSCVMSLKNRHVSKSS
CNYNHLDVDVNDLTMVEHTIDPEASFASTFQI1KKHALDLDRWQFKRSRLDQDKRKA
NTGSSNQDKAKSMSSPTEDEIEKMGFGEYSRSPTF

FIGURE 96

GGCCAGCGCGCGGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC
 CCAAGCAGCGCGGAGGAAACGCCGCCGCCACACCCCTCTCGGTCGCCCGGGCGCTGCCACCCCTTCCT
 CTTCCCGCGCTCCCGGCTCGCGGGCAGTCAGCTTGCGGGTTCGCTGCCCGGGAACCCGAGGTCACCA
 GCGCGCGCTCTGCTTCCTTCGGGCGCGCGCGCTCCACGCGCTCTCTCCCGTGGCCGGCGCTGGCACC
 GGGGACCGCTTGCTGACGCGAGGGCCAGCTCTACTTTTCGCCCGCGCTCTCTCGCGCTGCTCGCTCTTCAC
 CAACTCCACTCTCTTCCTTCAGCTCCACTCGCTAGTCCCGACTCCGCGAGCTCGCGCGCTGCGCGT
 CGCGCTTCGCCGTCGCCCTCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACATGGCAACGGTTCCGCTTGC
 CGCGCTTCTCTGACCCCTGGCAGTGCTCAGCGCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTGCAGCGCTTTACGTGTCGAAAGGCTTCAACAAGAACGATGCCCGCTCCACGAGATCAACGCTGATCAT
 TTGAAGATCTGTCGCCAGGGTTCTACTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGAATCATTTGCAAGCTGTCTTTGCTTCAGCTTCAAGAAGTTTG
 ATGAATTTCTCAAAGAACTACTTGAAGTGCAGAGAAATCCCTGAATGATATGTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCTCCTGGAGCGGATGTTCCGCTGCTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT
 CGCAAAATTGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTGCTCAAGGCTTAGCGTTGCGGG
 AGATGTCGTGAGCAAGGTCCTCGGTGTAACCCACAGCCGAGTACCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACTATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTCATAGATGCTATGCTGATGTTGGCAGAGAGCTAGA
 GGGTCCCTTCAACATTGAATCGGTGATGGATCCCATCGATGTGAAGATTTCTGATGCTATTTATGAACATGCAAG
 ATAAATAGTGTCAAGTGCTCAGAAGGTTTTCAGGAGTGTGGACCCCCAAGCCCTCCAGCTGGACGAAT
 TCTCGTCCATCTCTGAAAGTGCTTCAAGTGTGCTGCTTCAGACCACTACCCCGAGGAACGCCAACACAGC
 AGCTGGCACTAGTTTGACCGCACTGGTTACTGATGTCAAGGAGAACTGAAACAGCCCAAGAAATTTGCTGCT
 CCCTTCGCGAGCAAGTTTGCACAGTATGAGAGATGGCTCGAGGAACCGCAATGAGGATGACTTTGGATGGG
 AAAGGCAAAAGCAGGTACTCTTTTCAGTGACAGGAATGATTAAGCCACAGGGAACACACCCAGAGGTCGA
 GGTGACACCAAGCAACCAAGCACTACTGATCCTTCGCAAACTATGCTCTTCAGTGATGACCAATGCTGGGAGAGTGGCAATGA
 AGATGCAATCAATGGGAACGACCTGGACTTCTTGATATCAGTGATGAAAGTGTGGAGAAAGGAGTGGAGT
 GCTGTGAGTATCAGCAGTGCCCTTCAGACTTTGACTACAAATGCCACTGACCAATGCTGGGAGAGTGGCAATGA
 GAAAGCCGACAGTGCTGGTGTGGTCTCGTGGGCAAGGCTACCTCCTCACTGTCTTCGATCTTGTCTCTGG
 TTATGACAGAGAGTGGAGATTAATCTCAACTCTGAGAAAAGTGTTCATCAAAAGTAAAAAGGCACCGATT
 ATCACTTTTCAACATCTAGTGACTTTGCTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGC
 CACTGGTTTAAAGAGTCTGACTTTGTTTTCTCATTCAGTTTTGGGAGGAAAAGGAGCTGTGCATTGAGTTGGT
 TCTGCTCCCCCAACCATGTTAAACGTGGCTAACAGTGTAGTACAGAACTATAGTTAGTTGTGCATTTTGTGA
 TTTTATCACTTATTTTGTGTTGATGTTTTTCTCATTTTCGTTTGGGTTTTTTTTCCAACTGTGATCT
 CGCCTTGTTCCTCAAGCAAAACAGGGTCCCTTCTGGCAGTAACATGTACGTATTTCTGAAATATTAAATA
 GCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAGAAAAAGCCCCAAAAAGC

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FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVVGNVNLEEMLNDFWARLLERMFRLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMNAYNGNDVDFDISDESSGE
GSGSGCEYQQCFSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTGCGCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCCACAGA
AAGCCAAACAAGCATTCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACCTACCAGACACTCTTCTTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCACTTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCAGGAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTCAATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTCATCAAAGTGAACATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTTGCTTTTAGAAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

101/330

FIGURE 101

MAVLVLRRLTVVLGLLVLF LTCYADDKPKDPDDKPDGSKDPKPDFPKFLSLLGTEIIENAVE
FILRSMRSTGFMEFDDNEGKHSSK



FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGCTGCTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGGCAACTTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTCTGTGTCAGAGCCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCATGCGT
 CTCTAGGAACCTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

[illegible][illegible]

FIGURE 104

GTGGGATTTATTTAGTGCAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTAGCACAACAATCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCTCGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAA
 AAGTAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTCCTCAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTACGCCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACCAAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGTGCAAACCTGACGGAATGGAAACGACAGAATATAACTA
 ACCAACTGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCCCTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGTTCCAGTGTGGAAGCAGATATTACCTCAGTTTGTAA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTTGGGAAAAATGGTATATTCAGACCCACAGGCAAAATCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGAAGCAGAAATTGAAGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCCTTACGGTA
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAAACTGCCCTGTCTGGCAGTC
 AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT
 ACTACAATGCTGAATGACTGGAAGAAGAAGTATGCTAGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAACCTGCTGTTGGTTTTAATTTGTAACTGTGGCTGATCTGTAATAAACTT
 ACATTTTTC

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGATAAINSIOHNTRS NVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKV KEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDD VIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQ NITNQLEKWMKLNVEEGLYSR TLAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKA AKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 106

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATT
CAGGAATTNTAGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTCGGGGCGGGGCTGCA
 TCCGCATCTCCTCCATCGCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCGAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAAGAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACCAAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAC
 CTGACGGAATGAAACGACAGAATATAACTAACCAACTGGAAGAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAAACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT
 GCTGGAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTCCA
 GACCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAA
 CAGAATTTGAAGTGAAGCAAGCATTTCTCAGGAAGTCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAGAAAGATGTGTGCTAGT
 GTAAGATGACAACTGCCTGTCTGGCAGTCAGCTTCCGAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAGAAAGAA
 CTGATATGGCTAGTTCACTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAA

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCTCACCATTTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTCTGCTGTCTATGGGGGGAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTGTGCTGCTGCTCTGGGTTCATCCTCTGCTG
GGCTTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCTGTCTCTGAGAAGGCCCCACCACCCAGAAGCCAGCCATGAAGGCAGTACCTGC
TGCAGCCCTGAAGGCCCTTGCCCTAGCCTGGAGCCAGGACCTTAAGTTCACCTCACCTAGAG
CCTGGAATTAGGATCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTTGAGCCAGCGGCCAGAGTCTAGCCAGCTTGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTTACGTTGGGGAAGCAAATGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCTAGGCTGTCTCCAGTGTCTGCTGGATAATAAATGGAATATGGCTCTAA
AAAAAAAAAAAAAAAAAA

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGCCCTCAAACACCTGAGTGCTA
 CTCCTATTTGTCATCTGTTTGATAAATGATGTTGACACCTCCACCGAATTCCTAAGTGAA
TCATGTCGGGAAGAGATACAATCCTTGCCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTCATCACACCCTTCTGGTTCACATTTTCATTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA
 TCCACAGGCATCACGGCAGTGTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTT
 GACAGTTGAGCTTTTCCAAATCACAATAAAGCCATCAGCAGTGTCCCTTCCTGCTGTTCC
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCT
 TTCGGGCATTCCGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGCGTGCAGCAAATGACTATAGCTGGGGCAGTGTTTACTTGTATTTCACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTCTTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAACTCTCTGTGGTGAGGATTCCGAGAATCATTTGTCA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCAATTTGTCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAAGTGTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTGTTGGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCATTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGAAGGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTAAAGACCTAATAAACCTATTTCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTTLLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLKRRIKLTVELFQITNKAISSAPFLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

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FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCTCTT
 AGAATAATTTTGATGGGATTTGTGATCGAGGAAAGCCTAAGGGAAAAAGAAATATTCATTCTG
 TGTGGTGAATAATTTTGAIAAAAAAAAAATGTCCTTCTTCAACAAGGCTGCATTCTGATATT
TATGAGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCTTGTTTTGGCTGG
 TGACTGGAGTACATTCAAAACAAGAAACGGCAAGAAGATTAAGAGGCCAAGTTCACTGTG
 CCTCAGATCAACTGCCATGTCAAAGCCGGAAGATCATCGATCTGAGTTCATTGTGAATG
 TCCAGCAGGATGCCAAGACCCCAATACCATGTTTATGGCACATGACGTGTATGCATCCTACT
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGTGTGCTTGATAATTCCAGGAGGGAAAAATCTT
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATCCACCGGTGTCCAATCGTT
 ATCCCTACCACGATGGAGAAATCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGTGTAAC
 CCTACCCTACGCTCTTACATACTCATCTCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGCCTATCAGAGGCCACTATTCCAGGGACAACATGCACAGCGCGTCACTCTGATGCA
 GCTTCTGGCTGTACTGTAGCTGTGGCCACCCACACCTTGCACAGGCCATCCCCCTCTGT
 CTGCTTCTACACACGATCCCCAGACCCACATAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCATGCCACCTACACAAGCAGCCAAAACAGGCCACAGGCTGATCCAGGTATCCA
 AAGGCAAGATCCTTCAGAGCTGCTTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGAC
 TTGTTCCAAAGAGAAATGAGCACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTCTTTTAAATTTGAGGAGCACCAGCATTTGGCAACCGCGATTCCG
 AATCCAGAAGCAGTCTCTGGCTGATGTTGCCAAAGCTCTTGACATTTGGCCCTGCCGTTCCAC
 TGTAGGTTGTCTCCAGTATGGAGACAACCTGCTACTCACTTTAACTCCAGACACACAG
 AATTCTCGAGATCTGAAGACGCCATAGAGAAATTACTCAGAGAGGAGGACTTCTAATGT
 AGGTCCGGCCATCTCCTTTGTGACCAAGAACTTCTTTCCAAAGCCAATGGAAACAGAAGCG
 GGCTCCCAATGTGGTGGTGGTGTATGGTGGATGGCTGGCCACCGCAAGGTGGAGGAGGCT
 TCAAGACTTGCAGAGAGTCAAGAAATCAACATTTTCTCATCACCATTGAAGTGTCTGCTGA
 AATGAGAAGCAGTATGTGGTGGAGCCAACTTTGCAAAACAAGGCCGTGTGCAGAACAAACG
 GCTTCTACTCGCTCCAGCTGCAGAGCTGGTTTGGCCCTCCACAAGACCTTGACGCTGAGAT
 AAGCGGGTCTGCGACATGACCGCTGGCTGCGACAAGACCTGTTGAACTCGCTGACAT
 TGGCTTCGTCTCAGCGCTCCAGCAGTGTGGGACGGGCACTTCCGACCGCTCTCCAGT
 TTGTGACCAACCTCACAAGAGTTTGAGATTTCCGACAGGACACGCGCATCGGGGGCTG
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTCCGACAAGTACAGCAGCAAGCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACAGCAGCGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAGAGGAAGTTAATGATCCTC
 ATCACCAGCGGAGGTCTTACGACGAGCTCCGGATCCCAAGCATGGCTGCCATCTGAAGGG
 AGTGATACCTATTGGGATAGGCGTTGCTGGGCTGCCCAAGAGGAGCTAGAAGTCAATTGCCA
 CTCACCCGCGAGAGACCCTCTTCTTTGTGGACGAGTTTGACAACCTCAGTATGTC
 CCCAGGATCATCCAGAACATTGTACAGAGTTCAACTCACAGCCTCGGAAT**TGA**ATTACAG
 CAGGACAGACCCAGCAAGTGTGCTTTACTAAGTACGCTGTTGGACACCCACCGCTTAA
 TGGGCGCAGCGGCTGATCAAGTCTTTGGGCGAGGCTGGAGAAACAAATGCTCTTTGTTATTA
 TCTTCTTGGCATCACTCTTTTATATTTCCAAAACCTTGGAGTTACAAAGATGATACAAACGT
 ATAGAATTGAGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAATT
 GTTTTCAAAATGTTCGGAATACAGTGCAGCCCTTACGACAGCTTACGTAGAGCTTTT
 GTGAGATTTTTAAGTTGTTATTCTGATTTGAACCTCTGAACCTCAGCAGTTTCATTTTT
 GTCATGACAAATGTAGGAATTGCTGAATTAATTTAGAAGGATGAAAGATAAAAAA
 AA
 AA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC
 PAGCQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
 SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMO
 LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
 RQDPGGAAFQKPVGADVSLGLVPKEELSTQSLEPVS LGDPNCKIDLSFLIDGSTSIGKRRFR
 IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV
 GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
 NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTQLPLVKRVC TDRLACSKTCLNSADI
 GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDRIGAVQYTYEQRLEFGFDKYSSKPD I
 LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
 VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRIIQNICTEFNSQPRN



FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
 TGCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGAATGTCTCAGAATCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACTCC
 TCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACT
 GTGTCCATGCCAGTCTTCCAGTCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTCCGGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTGACCCCAACCACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA
 CTTCTCAGCTGCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTT
 AGACTCCTCA~~TAA~~ACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDFAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLMAEEAARKL
LPAFQTPGTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMPVFSLEAYWPLQSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPPTLELGRDAVESIEKISKVECG
FATIKDLRDHKL DNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAAATGCTTTATTTTGAAAAGAAACAATGTTCTAGGTCAAATGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGTCTACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGTCCACTGTTCTGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCTCCAGACACCTTGAAAATAACCAATTACCCCGAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCA**TAGG**TTTGGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGCATGCAATGAAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGTCTAAACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCAGAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTCACAGCCCACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTTGGTAAAGTACAGAATTGAGCAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFMTVLEEIIWTSLFMWWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIWIPSSWCSLTEGPECDDVTDITATVPYNLRVRATLGSQTS AW
SILKHPFN RNSTILTRPGMEITK DGFHLVIELEDLGFQFEFLVAYWRREP GAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPLV LALFAFVGFM LILV
VVP L FVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTAATACTGTCGAATACAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAGAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGGCTGGGTTGAT

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FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGTGGCGGGCAGCGGTGGCAGCGGCGTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGGCGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCGCGGCACCTACAGTGTCTCATTTCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCCTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACTGTGTGTCAGTGGAGGAGGTGAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTTAATAACCACCGCTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG
 AGACCCACTGACTCTCCTTCTTTACTCTTATGCCATTGGTCCCATCATTTCTGTGGGGAA
 AAATTCTAGTATTTTGATTATTGAATCTTACAGCAACAAATAGGAACCTCGGCCAATGAG
 AGCTCTTGACCAGTGAATCACCAGCCGATACGAACGCTCTTGCCAACAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGTCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCAGCATATAAAATAAAAATGAAAGTATCCTCCTCAAAA

FIGURE 120

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ
HYRALQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSGKEPTWNFWKYLVPDGGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GGCTGTCTACGTGCGGGATGC
 TGGCGCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGGCTGGGGGCCGGGGCCGCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCCCATCGGAGGCCCTCAGCTACGTTCAGGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCAGAACGAGAGGGCC
 TTGGTCGTCTCCATGAAGACGTACGTTGACCTTTGCCCAACTCAAGGAGGAGTTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCCTATGCATGGGTGCTCATGCAAGTTGGCCACCGCCAGCGGGCATCATTTCTGGTG
 TCTGTGAACCCAGCCTACCAAGGCTATGGAAGTGGAGTATGTCTCAAGAGGTGGGCTGCAA
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCCCTTTGCCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCCTGTCTGCCCATG
 ACCCCATCAACATCCAGTTTCACTCGGGGACAAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTTGTCAACAATCCAACTTTTAGGAGAGCGCTGAAATGCATGAGAAGAC
 ACCAGAGCAGTTGGGATGATCCTGCCCAACCCCTGTACCATTTGCCTGGGTTCCTGGGCAG
 GCACAATGATGTGTCTGATGTACGGTGCCACCCCTCATCCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGAT
 GTTCGTGGACATTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCTTGTCTGGGTCCCCTGACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTCGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCCGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGCTCATGTCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCACT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCGAGGAAGTGACAGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTCCGGCTGAAGGACGGGGAGGAGACCAGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTGTGCACAACTACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA
 GCAGATGGAACGACATCTAAGATCTG**TGA**ATAAAAGCAGCAGCCCTGTCTGGCCGGTTGGCTCT
 GACTCTCTCTGTGCAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTTC
 TGAGCCAGGCACATCAATGTCAAGGAATTGACTGAACGAATAAGAGCTCCTGGATGGGTC
 CGGGAAGCTGCCTGGGCACAAGGTGCCAAAAGGACGGCAGCTGCCAGGCCCTCCCTCCCTG
 TCCATCCCCCACATTTCCCTGTCTGTCTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRRERTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCKIVGRSKDMIIRGGENIYPAELEDFHHTHPKVQEVQVGVKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTCCGTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCACGATGTTCTGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGG
 GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTTCTGCTGGC
 AGTGCGGGGTTGCGGTTGCGGACTCCCCGCAAGAATGACCGCGCCTGGATCTTCACGGGC
 TTCTGCGGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGCGAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGATACATCGCCCGCGTCTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTTGCACTCGGGA
 TGGAGTAACAGGCCAGGGTTACGCTCAGTGGCTCCTGTTGCCAGGGGTCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCGGGTGCCCCCT
 CCAGAGCCCACGACTGTGGCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAAGTCCGAGACAGGGAGTAG
 AACACAGGGCTCCCGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
 CGCAGCAATTCAGGCGAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAATTTCCCTCTCACCTACTTCTCTGGCCTGGGTACCCCTCTTCT
 CATCACTTCTGTTCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTGTGTATGTTAGGACAGAGTGAGAGAAGTCAGTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCCGCATCTTTGGG
 GAATCGGTTCCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGV DVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGC FDGNVTLTAANVTV
SLPVRCGVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKMPAPTSTQTPRQGEHEASRDEEPRLTGGAAGHQDRS NSG
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL



[illegible]

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPRAPGDDEEAQVENLITANATEPQKQRTVQPSGGSLWNLRRLLLEPLDANVDA

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FIGURE 128

AAACTTGACGCC**ATG**AAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTCTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCTTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAG**T**
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA



FIGURE 129

MKIPVLPVAVLLSLLVLHSAQGATLGGFEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE
FLNWHALFESIKRKLPFLNWDAPFKLKGLRSATPDAQ

FIGURE 130

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTT
TTCTCCAGCCAGTTCCAACTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCACATATTAATTGTAACGATTAATAAAGAATAAGAGCAGCGAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGAATATGAATAACCAGAATCTATTTCCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGGCCATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTAGAAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGCGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACAAGAACA
 GACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCCTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAAAAGAAAAATCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGAAAAACCCAAACTTGTGTATGCAGAATACACCAAAAAAC
 CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAAATTAT
 TCCAAAAATGTTGAAAACGAAGTATAGTAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCTTAAAGCAATC
 ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCCATTTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA
 CTATTGCTGGAATTTGTGAAATTTATCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG
 AAACCCCTATGGGGTTTATGAAAAATACTTGGGGATCATTTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYREND CMFSPRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLEFNFRGVAASFRFKHLFLCGSLVFHVGDWEWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL



FIGURE 134

CACCCCTCCATTCTCGCCATGGCCCCCTGCACTGCTCCTGATCCCTGCTGCCCCCTCGCCTCTT
 TCATCCTGGCCTTTTGGCACCGGAGTGGAGTTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTTGGGCAAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTACG
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGACAGCTGGTATGCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGTGCTGACAGTGCTGTGGGTGGTGCCTACCCTGGGCACGACCGTCTCCTCCTTGCT
 TTCCTCCTTACCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCCACTGAATTCTAAATCCTTAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA
 CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACCTCCCCTGGCACTGTTACTTGCCCTCTGCGCCTCAGGGGTCCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCCTCACCACCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFVTSRPLLGIPESGGPDARQGWLAALQDRSILAP
LAWDLGLLLLFVQGHSLSMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPIPKGPV
LWEARAEFWATWVPLLCLFVLHVISWLLIFSILLVFDYAELMGLKQVYYHVLGLGEPLALKSP
RALRLFSLRHPVCVELLTVLWVVPVTLGTDRLLLAFLLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235



FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAAACAACAAAACCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCGGTTGACCTGTGGCTCTTCCGCTGGCTGCTCTA
 TCACGTGGTGTCTCCGACTACTACCCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGG**ATG**CGCTCGGCTCTCTGGACTGTCCTTCGAGTAGGATGTCAGTGAATCC
 CTCAAATGGAGCCTCCTGCTGTGCTACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCTTCAGATGTAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAACCATTATGGC
 ATTCAGGTGGGTAAGTGAATTTTGGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAACCCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCCAGAAGA
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTGGCAGGTCATGCTAAGGAACACC
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTAAATAAAGTAGGTACTGTGAAAAATTCATGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAAACAAAACAATGTAGAGTTTTATTATTG
 AACAATGTAGTCACTTGAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTTACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGAGTATTTTACAGTTATTATTATTATTTAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCATAGGTCAATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGATTAAAGCAAGAAAATCTGAAAA

MASALWTVLPSRMSLRSLKWSLLLLLSLFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTRLREHSNCSHQNPFVLIVTSHSPDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTLTIMAFRWVTEFCPNAKYVMKTDVFIN
TGNLVKYLNLNHNSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPFYCSGLGYIMSRD
LVPRIYEMGHGVKPIKEDDVYIGICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEITTFWQVMLRNLCTHY

FIGURE 138

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
 IWDYGNNGFAATRLFQKKTICIVHKMNKEVMPSIQSLDALVKEKKLQGGPGGPPPKGLMYSVN
 PNKVDLDSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174



FIGURE 140

CATTTCTGAACTAATCGTGTGAGAACTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG
 CTCATATATAGGAAATCGCATATGGTCCTAGTATTAAATTCCTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTTATATGCTAGAAATAGAGGATGTGAAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTCATG
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAGCAAAGGGA
 TTGAATCCGGATGGAAGTCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTATGTGAAGACAG
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTCAAGTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGCGAGGCACAGGCG
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAAACATTAAACGCAAAGTATTAGGATTGATTTCTTGAACCCCTCTA
 GGTCTCTAGAACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAATAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTTCTGTAATAATGATGGTGAAT
 ATACAGATAAAATGACAGACACTGTTCTATTAAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACITTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAATAACAAT
 CTGTGTTTTTCTAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIEIETLRLY
TRKKPNYELLEKEVEKRRVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPI SINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKKSRSRSQ
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKS KHHGGSRSRSGHGRHR

FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAACAGAAGAAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTCCTCC

FIGURE 143

GGACAGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGTC**ATGGC**
 GGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTCGCCTTCTTCTCGGAGTACCAGTGG
 TTTGTGGACTTTGTGTGTACTCGGGCGCGCTGTACCTCTTACAGAGGCCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCCTTCTTCTTCTGCTGCTGGCCATGCTGGTGAAGTGGTGCG
 GGAGGAGACCTTCGAGCTGGGCCCTGGAGCCTGGCTTGCCAGCATGACCCAGAAGTTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGAGCGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCAAGCTTCCTGTCTCCCCGTTCATCTGTGGCTCTGGACAAAGCCCATTCACACGGGAC
 TTCCTGCACCAAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCGGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCCTGGGCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCTTGGGTGGCTGCTTACTCCCCCTTCTCCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCACCAGCACTTGGA
 GGCTCC**TAGT**GCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGGCCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTCACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCCTGGGCCCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTF AFLFLLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGWDPVAKLAIRVGLAVVGSVLGAFLTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSQYLTPLILTLCNTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAAQCQLLASLFGLYFHQHLA

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTTCCTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAACTGGCTT
 AATCTGAAGGTCTTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTTAAGGAGC
 TTGGCTGGTTTGGGCCCTTGAGCTGACAGAAGGTGGCCAGGGGAATGCAGCAGACTGCTCGGAGAATCAGG
 CGCTTCTGTTGGCTGGTCTTGCCCTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACTCGCACTTCTCTG
 TATTCAAGACTCTGTAAGGTGCTCCCACTACGGCTGACCAAGATAGGAAGAGGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCTCCCAAGAGTTCTGCAAGCTGCCACCATCTCCCTTAA
 TGACAGACGAGCCTGGCTAGACAACCTCGCTACGTGTCTCGGCAGAGGACGGGAGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCAATTA
 AAAAATAAATCAGAGCTTTGAGTGTTCTTCAAGAGCAAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCAGCAGG
 GCAGGGAAAATTCTGAAAACACCACTGCCCTGAAGTCTTCCAAAGTTGTACCACCTGATTCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCCAAGTGAAGCCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTATCGCCAGAGACGGCCGGCTACTGCCAG
 GAGCATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGGCTCTCTCGCG
 CAGCCCTGCCAGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGAGCAGGAACAATGGACAGGCCCC
 GGATGCCACAGCCCCGAGATGACAGCTTTCATGTGATCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGAA
 TAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGGTGTGTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAG
 TCGCGCTCATCTGATTGAGGCCAGTGAAGACGTGTTACCTCGTCTGTGCCGCCAGGTTGGCAGCGGAGCC
 CTGACATCTTTGAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCATCTACAATTACTTGTGATGAGAAGTGGTAAATATCCAAAAGAGCCCGGTGAATCTCT
 CGGCATGACCGTCGCGAGGGGAGCATCAGTAGAGAATGGGATTGCTTATCTATGTCATCAGTGTGAGCCCG
 GAGGATCATTAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTTGAATGGGATGGGTCGAATGACA
 GAGGTGAGCCGAGTGAGGCACTGGCATTATTGAAGAAGCACTCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGATGATGAGCCCGAGGAGACTGCAAGCAGCCAGCAGCCCTGGACTCCAACCACTACATGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTCTGTGGCTGGAATTACCACGGTGTGTATAACTTAAAGATATTGTATTA
 CGAAGAACAACAGCTGGAAGTCTGGGCTTCTGCATTGAGGAGGTTATGAAGAATACAATGGAACAACAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACCAAGCATCAATGATGGAAGAATAGATGGTGATATTCTCTCTG
 CTGCAATGGTAGAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGACTTAAAGGAAGA
 ATTACTCTAACTATTGTTTCTTGCCCTGGCACTTTTTCAGCAATCAATGATCGGTCAAGGAAACAGAAAA
 TCACAATAGGCTAAGAAGTTGAACACTATATTATCTTGCAGTTTTATATTTAAAGAAACATCAATTGT
 AAAAATCTGAGGAAGATGATGATCATTAATGAAGCCAGTTACACCTCAGAAAAATGATGATCCAAAAAATTA
 AAACACTACTGTTTTTTTTCAGTGTGAGGATTTCCTATTCTCTACAACATTGTTTATATTTTTTCTATTCAAT
 AAAAGCCCTTAAACCACTTAAATGATTGATTGTATACCCACTGAATTCAGCTGATTTTAAATTTAAATTT
 GGTATATGCTGAAGCTGCCAAGGTACATTATGGCCATTTTAAATTCACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACAAGAAATAATTTTTCAGAGTTAAA

FIGURE 147

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSAAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRENSSENTAPEVFPRLYHLIPDGEITSIKINRVDP
SESLSIRLVGGSETPLVHII IQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV
FI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESA AHLI QASERRVHLVVS RQVRQRS
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISR DGRIKTGDILLNV DGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRC DILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCA**AATG**TGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAACTCTGCAAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGTCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCATGTT**TAGG**ATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGTTTTACACTCAAAGTCAAATTAATTCTTTCCCAATGCCCACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNII SP SNNGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWWKYNPLE
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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GGCACGAGCCAGGAACATAGGAGGTTCTACTGCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGCGTCTCT
 CCACCTCAGGTGCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACCTTCACTCTGCAGGACAGAGGGGCGAGGCCCAAGGTTGGA
 GATGATCTGCCAGGCGTCTCTCGGGCAGCCCACTATCACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCTGCCG
 AGCCAGACATCGGACTGGTCTGGTGCCAGGCTGCAAAACAACGCCAATGTCCAGCACAGCGC
 CCTCAGAGTGGTGCCCCAGGTGGTGACCAAGAAGATGGAGGACTGGCAGGGTCCCTTGAGA
 GCCCCTACCTTGCCTTGCCTGCTCAGAGGACCCCGCGTCTGAGTGAAGAGAGTATTGGG
 GGGTTCAGGATAGGGAATGGGAGGTGACAGGACGCAAGCAGCAGCCATGCT**AGTA**ATGAAC
 GTCCAGAGAGCCAAGCAGCGCAGAGGACTGCAGGCGCATCAGCGTGCAGTCTGATTCTGATTGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAATAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVFFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNINVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPFITNSLIGKDGQVHLQQRPCRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**ATG**GCGAGCAGCCGCGCTACCAAGATCCTTCTGTGCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCTCACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTGAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCTGGGGAAGAAA
 CTAAATGTCACAACGGCCTGGAAGCACAGAACCAGTACTGAGAGAGGTGGTGACATACT
 TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCCTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAGG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCCCTT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGTCTACC
 TGATGGAATTCCTGCACCTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGTTGGAATAACAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAAAATAACGTTAGACTTCAGACCTCTGGGATTCTTTCCGTGCTCTGAAGAG
 AATTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCTCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
HYDCGNKTVTPVSPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCAATTCTG
GTGTGGCTTTCTTTGCAGAGGATTCACCTTCAAATCATGAACCTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCATAAAACAGGACAGATTATTAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGACAGCAAGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTTCATTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACCATGAAG
 CTCTTGTTGGCAGGTAACGTGTGCCACCACACCTGGAATGCCATCCTGCTCCCGTTCTGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGGCCCC
 AGAACTGCCCCCTCCGTTTGTCTGTGCAGTAACCAAGTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTGTGCAGT
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGCCCTCAAC
 ACCCTGGAGCTGTTTCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCCTCTTACGCCCTTCA
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGAGGGGCTGTTCAACTCAAGTATCTGAACCTGGGCATGTGCACCATTA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAAGGAACCACT
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCATG
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACCTGTGGAACCT
 CAACCTTGGCCCAATAAACCCTCTCTTCTTTGCCCCATGACCTCTTTACCCCGCTGAGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCATGCTCCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCTTCCAGTGCTCTGCCCCCT
 TCATCATGGAGCGCACTCGAGACCTCAACATTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTGTCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGTGCTGC
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGACGGCACTCCAACCGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAAACACCTCCAACACAGCTTCTTCCACAGT
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAGCCTGTTCTTA
 CCACGCTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCTATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACACGACGCGGAGTACAGTC
 ACAGCCGCCCGGACGTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCAACATCT
 ATGACCATATTAACTACAACACCTACAACACGACCATGGGGCCCACTGGACAGAAAAACAGC
 CTGGGGAACCTCTCTCACCCACAGTCACCACTATCTCTGAACCTTATATTAATTCAGACCCA
 TACCAAGGACAAAGTACAGGAACTCAAATATGACTCCCCCCCCAAAAAACTTATAAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTTGTA
 TATGCTTATATATTAAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLLEELEMSGNHFPPEIRPGSFHGLSSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSLPHDLFTPLRYLVELHLHHNPWNCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGvyTCMVTNVAGNSN
ASAYLNVSTAE LN TS NYSFFT V TVTETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLP TI HDHIN YNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

FIGURE 158

CGCTCGGGCACCAGCCGCGGCAAGGATGAGCTGGGTTGCTGGACGCAAGTGGGGCTCACTTTTCTTCAGCTCC
 TTCCTCATCTCGTCTTGCACAGAGAGTACACAGTCAATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG
 TGTCCGGAGTGCCTGAAATATGATCAGATTGAGTGCCTCTGCCCCGGAAGAGGGGAAGTCGTGGGTTATACCAT
 CCCCTGGCTGACAGGAATGAGAGCAATGAGTCTGACTCCTGCCCTGATCCACCCAGGTTGTACCATCTTTGAAAACT
 GCAAGAGCTGCCGAAATGCCTCATGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG
 TGGCCAGCAGGCTGGTACGGAGGAGACTGCTGCGATGTGGCCAGGTTCTGCGAGGCCCAAGGGTTCAGATTTT
 GTTGAAGACTATCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTTGTCTATCCAACCTAA
 GATTTCCTCATTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAGGTTCTGTATGGAGACAAC
 CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGCCAGCTCCTATCCAGAGCATAGGATCCTCACT
 CCACGCTCCTTTCCACTCCGATGGCTCCAAGAATTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT
 GCTCCTCATCCCTTGTTCATGACGGCAGCTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTG
 GCAGGCTATCTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAA
 TGGGTACCAGAAAATAACAGGGGGCCTGGGCTTATCAACGAGCGCATGCTAAAATTTGGCACCCTGGTGTGCTCT
 TCTTTTGAACAACCTCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGG
 AAACAGCCCATCTGCATAAAGCCTGCCGAGAACCAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGAT
 GCAGGTTCACTCAAGGGAGACACCATTAACACAGCTATACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTG
 CCCCTACCAAGAGCCAGCCCTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAG
 TATGAGTGCATCTCACCTTCTACCGCCCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAATGGAG
 TGGCGGGGACCATCTCGATCCCTATCTGCGGGAAATGAGAACATCACTGCTCCAAAGACCCAGGGTTGC
 GCTGGCCGTGGCAGGCAGCATCTACAGGAGGACCGCGGGTGCATGACGGCAGCTACACAAAGGAGCGTGG
 TTCTAGTCTGCGAGCGTGCCTTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGG
 GAAGTGCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTTACCGGGATGATGACCCGGATG
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTGCAATCCCAACTATGACCCCATCCCTGCTGATGCT
 GACATCGCCATCCTGAAGCTCTAGACAAGGCCCGTATCAGCAACCGAGTCAAGCCCTCTGCTGCGTGGCAG
 TCGGGATCTCAGCACTCTCTCCAGGAGTCCACATCACTGTGGCTGGCTGGAATGCTCTGCGAGAGCTGAGCA
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCACTGCTGGACTCGCTGCTGTCTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATACATGTTCTGTGCCAGCTGCGAACCCACTGCCCTTC
 TGATATCTGCACTGTCAGAGCAGGAGGATCGCGCTGTGCTCTCCGGGACGAGCATCTCTGAGCCAGCT
 GGCATCTGATGGGACTGGTCACTGGAGCTATGATAAAACATGACGCCACAGGCTCTCCACTGCTTCAACCAAG
 GTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTC
 TGTATATCCGTCTGTACCTGTGTCATGCGTGAAGCAGTGTGGGCCCTGAAGTGTGATTTGGCCTGTGAACCTGG
 CTGTGCCAGGCTTCTGACTCTCAGGGACAAAACCTCAGTGAAGGGTGTAGTAGACCTCCATTTGCTGGTAGGCTGTAT
 GCCCGTCCACTACTAGGACAGGCCCTTTGGAAGATGCGAGGCTTGAAGAAGTAAGTTTCTTCAAGAAAGACC
 ATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTGT
 ACCGGGAAGATCTGGGCTTCACTGAGGCCCTTTTGAAGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCC
 CAGGCGCAGAGCTGGGATGGTGCATGCTTTGTGTACATGGCCACAGTACAGCTCTGGTCTTTTCTCTCC
 CCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACACAAAAAATAAAAAA
 AA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 159

MELGCWTQLGLTFLQLLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSLHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNSYVLSGNEKRTCQONGEWSGKQPICIKACREPKISDLVRRRVLEPMQVQSRETPH
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAACHCVTDLGKVTMIKTADLKVVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCTGCAGTGAAGCAGAGAGATAGATATTATTCAGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCCACCTTTCTCTACAAATTCGGATTACTGTGTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCAGTAACACTCTCGTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTA AAAAGT
 TTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTTGGGAC
 TGCCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAATATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTCACGAGTCTGG
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCATTGACCCTGGATCTTTTGGTGATGTTGG
 AAGAACTGATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAAACAAGACAGCTTCTTCTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTCTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATCTCATTATCTCTGTAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCTGGCTGC AAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTA AAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAAATA
 TGCTCTACAAATACCTCTGTAGTAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLTFHLSYKFRLLLLLTLCCLTVVGVWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSYFGGVLTALSREQFFKVNG
FSNNYWGWWGGEDDDLRLRVELQRMKISRPLPEVGKTYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

CGTGGCGCGGGTCCGCGAGCGGGCTGTGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
GAGCTTCAGCTGCATTCCTCCGCGTCCGCGTCCGCGTACCGCTTCTCCCGCTCCGGGCGCCGCAATG
GCCAGGACGTTGGTCCGCCCTCGCGCGATCTCTTGGTGTCTGCTGCTCTCCTCGCTCGGCCG
CCCGGACGGGTGGCCCGCAGGCTGTGATGAATCAATCTCACCACCGATAGCCCTGCCACCA
CGGGAGCGGTGGTGACCATCTCGGCCAGCTGGTGGCCAGGACAACGCGAGCTGGCCCTG
CCCGCTGACGCCACCTTACCGCTTCCACTGGATCCACACCCCGTGGTGCTTACTGGCAA
GATCGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCAGCTGCCCGGGGAATTCCCGG
TCTGTGCTTGGGTCACTCCGCTGACTGCTGGATGTGCCAGCTGTGCCAGGGGCTTTGTG
FTCCTCCCCATCACAGAGTTCTCTGTGGGGGACCTTGTGTACCCAGAACCATTCCTTACC
TGTGCCACGCTCTATCTCCTAAGACCGTCTGGAAGTCTCTCTTCTCCTCCACGACCGGA
GCAACTCTCTCAAGACCGCTTGTTTCTCTACAGCTGGGACTTTCGGGACGGGACCGCATG
GTGACTGAAGACTCCGTGGTCTATTAACTATTTCATCATCGGGACCTTCACCCTGAAGT
CAAAGTGGTGGCGGAGTGGGAAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
CCGGGACTTCTCCGCTCGCTGAAGCTCGAGGAACCTTCGAGGACTCAAGATGTTGGGG
CCCACTCTAATTCAGACTTCCAAAGATGACCGTGACCTGAACTTCTCGGGGAGCCCTCC
TGTGACTGTGTGCTGGGCTCTCAAGCTGAGTGCTCCCGCTGGAGGAAGGGGACTTGCCAC
CTGTGTCCGTGGCCAGCAGCGGTACACCTGACCCACACCTTCAGGGACCTTCGGGACTAC
TGCTTCAGCATCGGGCCGAGAATATCATCAGCAAGACATCAGTACCAAGATCCAGGT
GTGGCCCTCCAGATCAGCGCGGTGCTTTGTGTTTCCCATGTGTCTACACITATCTAGCTGA
TGTGGGCTTTCATATGTACATGACCTGACCTCGGGAATGCCATCGCAAAAGAGCATGTGTGGAG
AACC CGAGGCCACCTCTGGGCTGAGGTGCTGCTGCCAGATGTCTGTGGGCTTTCTTGCT
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGTGAGAACACGGGCTGCTCCGCCCTCT
ATAAGTCTGTCAAACATACACCGCTCGAGGACTTCCCTCCCCACCCCATCTCAGTGTAA
CTAGCTCTGACTTGGAGTTTCCAGCAGGCTGGTGTGCACTTACGACGAGGGGGTTCATT
TGGCTGGGGCTGTGGCCTGATCATCTCCATCTGTACAGTTTCAGCACTGCCACAAGCC
CTCCCTCTCTGTACCCCTGACCCGAGCCATTCACCATCTGTACAGTTCGACCCATGACA
TAAGCCCCACTCGGTTACCAACCCCTTGACCCCTACTCTTGAAGAGGCTTGTGTCAGACT
TTGATGCTTGGGGTGTTCCGTGTTTCACTAGTGGGCTGGCTGGCCACTGCCCATGCCATTCCT
CTCATATTGGCACAATCTGCTGTCCATTGGGGTTCTCAGTTTCTCCCCAGACAGCCCTA
CTGTGCCAGAGAGCTAGAAAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC
ACATAGATTGGGCACATCACAGAGAGAAAGTGTGATCTGTACACACACACACACACACA
CACACACACAGAAATATAAACAGAGTGTGCATATGGGCATTTCAGATGATCAGCTCTGTA
TCTGGTTAAGTGGTGTCTGGGATGCACCTGCACTAGAGCTGAAAGGAAATTTGACCTCA
AGCAGCCTGACAGGTTCTGGGCGCGGGCCCTCCCTTGTGCTTTGTCTGTGAGTTCTTGC
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGCACT
AAATCTGAGTGAATGCAGAGTGCTTTATAAATACAGCTATTTTATCGAAACCCATCTGTG
AAACTTTCTACGAGGAAAAGGCCCTTGACGCGGTAGAACAGGTTGAGTCAAGGCGGGGCGG
TGGCTCAGCCGCTGTAATCCAGCATTTTGGGAGGCCGAGCGGGGTGATCACGAGATCAGGA
GTGACGAGCACCCCTGGCTAACACCGTGAAGCCCGCTCTCTACTAAAAAATACAAAAGTT
AGCCGGGCGTGTGTTGGGTGCCGTGATGTCCAGCTCATCGGAGGCTGAGGACGAGGAATG
GTGCGAACCCGGGAGCGGAGCTTGACAGTGAGCCAGATGGCGCCACTGCACTCCAGCTGA
GTGACAGCGGAGACTCTGCTCTCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWPAPAGVAAGLYELNLITDSPAATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDTQ
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTFRDPGD
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMC CGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

165/330

FIGURE 165

MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQFQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKT

165/330
MALSSQIWAACLLLLLLSLTSGSVFPQQTGQLAELQFQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCKT

FIGURE 166

CTGTCAAGGAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGACAGGTGCTGCCCTGGC
 CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTCTCTGGGC
 ATCTCCCTGACTGTCTCTTCAACCTCCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGGTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGAAACCTGCTGAGCAGAACCAATTATAAATTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGGGGGTTAGGAGTGCTGATTCCGTAAGTCTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATACTTGCCAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGC
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCAGCGATCGATGTGATCATCTTGCCACAGCATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGACTCATGGGTGTGATTCAAGAGACCATGGTGAAGGCCCTG
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAATACGGGA
 TGGTGAAGTACCTGCTGCGAATGATGACCAAGTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCGAGATGAAGATGCTGTCCAGTTTGGCAATAGGGTGAATCTGC
 CATTCGACAGGAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCCAC
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCAGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCCGCCGCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCCTCCGGCTGCTCTGGATCCAGGACTCCGGCTTTCGCCGAGCCGACAGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAATCCCCA
 CCTTGTGACCGCTGTGCGGGCTGAGTGGTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCCTGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGAGTGTGCTGGGGGCGGCCACCCG
 CTCTCCAGGAAGGACACAGCTGAGGCACCTGGGCTGGCTTCCGGCTTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCTATCTGCAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG
 GGCCGCTGACTGGGGCATGGGGAGAAGCTGTGTTCTGACTCCAGGCTAACCCCTGAACCTCCC
 ATGTGATGCGCGCTTGTGTTGAATGTGTGTCGCGTTTCCCCATCTGTAATATGAGTGGGGG
 GAATGGTGGTGAATCTTACCTCACAGGCTGTTGTGGGATTAAGTGTGCTGCGGGTGAGTGA
 AGGACACATCAGTTCAGTGTTCAGTACAGGCCACAAAACGGGGCACGGCAGGCCCTGAG
 CTCAGAGCTGCTGACTGGGCTTGGATTGTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIIVPAIFGV SFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRK GME
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGV LIRYCFLLPLRIAL AFTG
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RGGICVANH
TSPIDV IILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCINNTSVM MFKKG SFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
LRMMTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGG LVDLLWDGGLKREKV KDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
 CGTCTCCTCCAGGG**GATG**GCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCCTCCAC
 ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
 AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
 CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
 GCTCCCGGAGCTCTACATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
 AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGCGGGCTGT
 GTGTCTGCGCCAGGGGTGCAGCTAGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG
 GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCC**TGA**AAGTCCA
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
 CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCAACCAGG
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGACTTCCT
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
 TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGC AEEMEEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLP PGFKAQNGIAIMVYTNSNTLYWELN QAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTL LLAPGEFQLSGVGP



FIGURE 170

GTGGCTTCATTTAGTGGCTGACTTCAGAGAGCAATATGGCTGGTCCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCCGTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
 CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCT
 CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAGAAGAAGAGAGTGGACATTTGTGCGGAAACTCCTAACATATGCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAAATCCTAAAGGAAGA
 TCCAGCAAATACGGTTTACTCCACTGTGGAATAACCGAAAAAGATGGAATAATCCCCACTCAC
 TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG
 CACTCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVS RNFSPI LARKLCEGAADDPSSMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEEYIEEKKRVDICRETPNICPHSGENT EYDTI PHTNRTILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI



FIGURE 172

CTGGTTCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCTCT
GTGTCTCCTGTGTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAA
ACTCCTAACATATGCCCCCATTTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAATAATCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCCTTGGAGAA
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTGAGTTCAGACATCAAGGAAA
GGTTTGCACAACATATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTGATACACCCTTGACAAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 174

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
 IHVLENSLVLVKHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI
 NEKDGETFQLMGLYGREFDLSSDIKERFAQLCEEHGILRENIIDL SNANRCLQARE

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTCTCAAAACCCATCTCTTGCTTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCAC
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTtaggtctattgct
TGTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTCCITGGCTGTC
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAA

MTCCGEGWTS CNGFSLLV LLLLLGV LNAIPL IVSLVEED QFSQNPI SCFEWWFP PGIAGLMA
IPATTTMSLT ARKACNNRT GMFLSSFF SVITVIGAL YCMLISIQ ALLKGPLM CNSPSNSNA
NCEFSLKNIS DIHPESFNL QWFFNDSC APPTGFNK PTSNDTMA SGWRASSF HFDSEENK HRL
IHFSVFLGL LLVGILEVL FGLSQIVIG FLGCLCGV SKRRSQIV

GTCGAATCCAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGCT
GCCAGCTGTGCTTCTGAGATCAAGTCTTCTTATCTTAAAGTGAGCTGCGGTAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCAGATCAGATATCTTTTAAAGAAACGACTCTCATTTGAAAAGTCCCTGGTGGAAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCAAAGTCTTTCAACGACAA
CTGATCTTCACTAAAAATGTAAAGTTTCAACAGCTGTTCTTAATAATCACTGCGCTGC

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCTC
GAACTGTGACATGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

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FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC
 TGGCTGGGGCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACATGCCGCCGGCTCC
 AGTGTTTCCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCGCCACCCTCGGATGCTGAC
 GCCCGCCTTCCATTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGACGCTGTATCCGGGAGCGGCGTGG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGGCAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC
 TTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTCTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCGGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCCGAGAACTGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTTG
 CGTTGATGCTGCTGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTCACTTTCTGACCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWG
HLGLITPTEGLKdstQMSATYSQGFTVWLGPiIPFiVLCHPDTiRSITNASAAIAPKDNLF
IRFLKPWLGEgILLSGGDKWSRHRRLTPAFHFNILKSYITiFNKSANIMLDKWQHlASEGS
SRldMFEHISLMTLDSLQCiFSFDShCQERPSEYIATiLELSALVEKRSQHILQHMDFLYY
LSHDGRRFHRACRLVHDFTDAViRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEDG
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
DDLAQLPFLTMCVKESLRLHPPAPFiSRCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
PDPEVYDPFRFDPENSKGRSPLAFiPFSAGPRNCiQAfAMAEKVVLALMLLHFRFLPDHT
EPRRKLELiMRAEGGLWLRVEPLNVGLQ

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAGAGGAAATTTGAGAAAGTTTCAGGATT
CTCTGGACAAGATCCTTAACATTTTACTGAGTCATCTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCTGATTGCTTCTGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGTGAAAC
AGTGTGGAGAAAACTAGGCCAACTACACCCTGTTTCATTGTTACCTGGAAATAAATCCTCT
ATGTTTTGCACAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPILLSPLLDLSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTtagTtccCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
CCACCTCCGCCAGGAAGTGCAGGCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA
AGGGGCAGAGGATGAAGTGGAAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
CAGGGGTTcAGTACCAGCAGCACAGCCAGGCCCTGGGGAAgTTTCTTCAGGACATCCTCTGG
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCACACAAGCCTTACTCACCTCTCTCT
AAGTTTtagAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

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FIGURE 186

MPSPGTVCSLLLLGMLWLDLAMAGSSFLSPHQVRVQQRKESKKPPAKLQPRALAGWLRPEDG
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQOHSQALGKFLQDILWEEAKEAPADKO



FIGURE 187

CGGCCACAGCTGGCATGCTCTGCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCGTATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTCTTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCAGCCTGGGGCCAGAGTCTTT
 GTCCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCCAGAAGTGAGATCATGGACAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAACACAAGTAGAAATTCTAACATGAAATATATTACAGGCAGGTCACCACTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTGGTCATGGTGGGCCAGCTGCAAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGTGGGTCAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCTGCCCTGCAGTTGTGGCAAGAACGCCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTTCATAACCACAGGTACCCCTACAAACCACTGTCCCACACAACCTTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MNTWLLFLPLFPVQVQLTIVIIIGMLVLLLDFLGLVHLGQLLIHFIYLSMSPTLSPRPQGW
VVRAAHLTPLLEYVPNPPEPTPGARVFPVPRVMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAEITPRPAGVVPGA

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCCAGGGAGAGGTGCCGAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCCTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTTATGGCTG
 GGCTTCTACATGGCTGGCTCTCCTTCACTGCTGCATGGCGTGGCTGTCAACACCTTCA
 ACAGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACACATCACCATCAGTGTTTCCCTCGGGCGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGA
 GTAGGCTTGAGCCCTACCTTACAGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCCTTTGAGCATGGTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCATGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDINTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFPCPVRSPGDGGPHDVFTSLPSDCQLGSRRLLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDINTSTQEVVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFPCPVRSPGDGGPHDVFTSLPSDCQLGSRRLLETTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCA**GATG**TGGTTACCCCTTGGTCTCCTG
TCTTTATGTCTTTCTCCTCTTCTATTTCTGTCACTCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCTTCCCTGCCCCGCCGTAGATTGAG
GACATTCGCCCTGTGTGCCACCAACCAGGACTTCCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAATGAGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTTGATTCCAAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPILSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

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FIGURE 193

GTAGCGCGTCTTGGGCTCTCCGGCTGCCGCTGCTGCCGCGCGCCCTCGGGTCTGGAGCCAGGAGCGAGCTCA
 CGCCG**ATG**GCAGCGCATCAAAAGCTTTGATTAGTTTGTCTCTTTGGAGAGCAATCGGACCTGATGTTTTGATGCTT
 GGATTTGGCCCTTCCAATATACAAATACTGGCCCTCTTTGTTCTATTTTTTACATCCTTTTACCATTATCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGAACTTCACTTCCTTC
 TTACAACGGSGCATTTGTCGTGTACGCTTTTGGACTCCCTATTGATTTGGCAGAGCACATCTGATGTAGTGGGGA
 GCTTGTGCACCTTGTCTCACAGGAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGGAG
 CAATGACGACTTCAGCTGGCAGCAGTGC**TGA**AAAGAAATTAAGTAATGTTCAAAATGGACTTCCTGTCAATTT
 GTTGGCCATTACAGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTGGGGGTATTTA
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGTGTAAGGATTAAGAGGATTTTCT
 CTTTGGAAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTATGTGTTTTCTGTGTAGGTTGATTTTTTTGGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTGCATTTGGTAGGAATTGCAATTCGGCCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATATT
 TAGCCTCCATTATTACAAAATTTATAAAAAATAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATCTCAGTGCAATATAGCTGCATTTATACCTCAGAG
 GGGCCAGTGTAAATGCCCATGCCCTCCGTTAAGGGTGTGTGGTTTTACTGGTAGACAGATGTTTTGGGATTG
 AAAATTTATTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCAATTTAGAGAATTTATGTTAACTTTA
 AGGTAAAGGTGTAAAAACATTTTGAGATAAGGTTTTATTATGTTATTATGTTAGAGTGAAGTGCATGT
 GGGAGAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGTATCTCCTATC
 AACCTTTTATGTTTTACCTGTAAATGGACATACATGGAACCACTACTGATGAGGACAGTGTGATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTGACTTATTTGGTATGTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTATAACACTTGAAGTGTTTACTTACCTGAAAAATTAATGCTATGCCGTACATT
 CAGAGTGCCCTTCCCTGCAAGGCCCTTGCATGATTAACAAGTAACTTGTAGTCTTACAGATAAATTCATGCA
 TTAACAGTTTAAAGATTAGACCATGGTAAATAGTAGTCTTATATCTTAAGGTTATATCATATGTAATTTAAAG
 TATTTTAAAGCAGTTTCCAGTAACTCTGATACCTCTGAAGTGTGTTGATTTGAGTCTATCATGATAGATCTGCTGTT
 CCTTATAAAGGCATTTGCTGTGAGTTAATGCNAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAACAT
 ACCTGACCAAAAAATCCAGTAAACAGGCAATGATCAATTTATAGTGGTCTTTACATCTAATAAATATCAGGA
 CTTTTTTCAGAGTGGGTTATAAAAAATTAAGTTGGTCTGACAGTATTTTGTAAAGATATTTGTTGTATG
 TTTATTCAGTATATCTACATAAAAAATTTATTCGCCATCAGCCAAACTCAGTAATCATGACAGCTGTCTGTGT
 TTTATGAAGTTTATTTCTCAGAAAAATGGGAATAAATTTGGGATTTGTTGAGCTTTTTTACTRAAGATGCTTAA
 AGCCACAGSTTTATTCGCTAACTTAAGCCATGACTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG
 GCCTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTGTGGTATTATAATGTTGAGATTTCAAGAGGAA
 GGTGCAGGTACACATGATTAGAGAGCTGGTGAGACAGTTGGGAACCTTTGTGCTGTGTATCTACTGGACTTT
 TTTTTCGAGGAAGTGCAATCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTGAGTGCAGTGCAGTGCCTGCTG
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTTTCTATATACTAATTCGATTTGGCAGCATT
 GTGCTTTGACCTTGTATACTAGCTTGACATAGTGTCTGCTTGATTTCTAGGCTAGTACTTGAGATATGAAT
 TTTCCATAGAATATGCACTGATACAACATTAACATTTCTCTATGGAAAGAAACCTTTGATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAAATAA

CACGGCTGCGCGCCAGCAGCTCCGCCGACGGCTCCGCACACGGCTCCGCCACGGCTTCGGACACGGCTCCGCC
 CACGGCTCCGGTGCACAGCTTCGGCGCGACACTGCTGGTGGAGGGAAGGAGCGCGGGCGCTCTCCGGCTCGCT
 CGCGCGCCGGTCCGGCGCGCCAGCTCCGCCACCGCGCGCGCGCGCGCGCGCCGACGAAGCATGAGTGCAGCGCGCTC
 TCTCGAGCTCGCGCGGGCGCGGAGTGGCAGGCTGTTTCCGCGAGGTAAAGAGTGGCGCGGTGACAGTGGTCTGTTCC
 CAATGACGACCATTAACAGCACTTCGCAGATCTCGGGGATTCGCGAGGCCGCGAGTTTGGAGTTTATTTCCGCCAC
 AAGCTCAGAGCTCGGAAGCTCGAGGAGGAAGGAGGCGCGGAGGAGGCGGAGGCTCGGGCTCGGCGACAGTGTGG
 GAGAGCATTTGCGCGCTCGGCAGATTCGCCGCGCGCGCGAGCGGGGCTGGCGTGCAGACACAGCGAGACAGT
 GCGCTGCATATAATTAGCTGTCACACAAGGAGGACAGCTGATGAGGAGTGTCTCACTCTCGAAAGAGGATTTCT
 GACCGAGGCGTTCCAATTGACATCTTCAGTCTCTCTGGAAGATTTCTCGCTCATGCACTTTCCTGTCTCGCTGCT
 CTCGTCTATACTGGGTCTGGAGGAGGCTCTCGGGGGTGGCTGTGTCTGTCTGGGGGCGCTGCTTCAGATCT
 CGCCCGCGCGCCCGAGCGGGTGCGCCGAGCTTGCCGCTGTCGAGGGGGCGCTGTGTAATCGGAGCGCGTCAACC
 CACACGAGGCGCGCCACCAACTGTTCGCGCTGTCTGGGTTGTCTCGGCTACACAAGGCTCTCGAGAGTTCGCG
 GAGCGCTCTTCAGAAATTCGGCGAGTTAAGGATTCGAGTCTGAGTCTGAGTCTGAGTCTGCTCTCGCTCGAGG
 CCACCTTCGCGCCGATGCCCACTTCGCGAGCTGGACCTGCTGCTGACACAAAGCTCGAGCGGCTCTCGCGCCAG
 CTCCTCGACGGGCTCGGGAAGTCCACCGGCTCATATCGGGCGACGCCCATCAAGTTTGGCGCGCTGCGAT
 TCTCAGGAAGTCGCGAGCTCAAGTTTCTGCATCGATCGATCAATCAGTCTAAGATCTGGGCGCAAGCTCTTT
 TCGCGCGCTTGTCTTAAGCTCAGAGGCTCGACCTCGAGCAGCAAGCATTGGTCAAGTGTCTCGGCCATCT
 CGCGGCTGCTGCTCGCTCACTCGCTTCGCTCGGAGGAGCAACAGGTGGCGATTTGCTGACGTCTCGCTGGAAGT
 GCGCGGCTGCGCTGCGGAG
 TCGCGCCACTGCAGCTCTCTCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT
 TCGCGCCACTGCAGCTCTCTCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT
 AAGTCCCTGACAGCATCACCTTCGCGGGGAAGTCTGGGATTCGGGGCGCAAGCTGTGTGCTGCTAGCTCTGTG
 CTCGACCAACTTCAGGGGCGCTACAGTGCACATTCGAGTGCGCCAGCCCGGAGTACGCACAGGCGGAGGAGCG
 TCGTGCAGCGCGTGCACGCTTCCACTGTGCGAGGATTCGAGGCGCGAGCGACCGTCCACGCGCACTGCTCTCGCC
 GTCCACCAACCGCAGTGATCTGGGGCGCCCTCGACAGCTCGGCCACCACTGCTCGGAGACGCGCGGAGGGGAGCA
 AAGTGTCTCATCTGAGCTCGCCACCTGGCTCTTCAGCGCGCGAGACACGCGAGAGCGCGCTGCAGATCACCA
 AGGTGTCTCATCTGAGCTCGCCACCTGGCTCTTCAGCGCGCGAGACACGCGAGAGCGCGCTGCAGATCACCA
 GTTTTCCAGCGAGCTCGAGCAGCTCAGACAGCTTCTTGTACCGAGCGAGGAGCAAAAGCAGAAACAGAC
 CATGTACAGATGGTGTGCATCTTCTGCCAGGATATCTGTTGATTATAAACCGAACCAACTTGAAGGAGCGC
 TGTGATCATCAACGAGTATGGCTCTGTGCTATCGCCACGAGCAGCCGCGAGGGAATCGAGGTTGTGAATTGCT
 CAGTGGCTCTCAACCGCGCTACCAAATAGCCTTGGGACGCGGGAAGCGCGCGGCGAGCGTGGGT
 CTCGCTGCTGTGCTCGATAGTCTCTCTGTGCTGAATCTTAAAGGGGATCTCTCCGAGACATTCGACATTTAG
 CTCTCTGCTGTGCTGATTAAGGCGGAAATTAAGACACAAACCAACCAACCAACCAACCAACCAACCAACCA
 TATCTTAATTAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
 AAAGTGGCGCATTAAGACAGAGAGAGAAATCTCTGCTTTGTTTATGTACTCTCCCACTCCGCATGATTA
 AAGCATCATGATCTATAGAGATCTTAAGTCCATACGATTCATGAAGAACCATTGAAGAAGGAATCTGCAATC
 TGGAGGCTTAAGAGCAAAATGATGACCATAGAAGAAATGTCTTACTTTGTGTGTGTCTGTATGTTCTGTG
 TGGTGTCTTTGTAGAGTGAACAAGCTTGTCTACACAAACGGGAATTTAGTCACTCATCTTTCAGCCCTGT
 TGGTGTCTTTGTAGAGTGTGGTGGGAGGTGGGGGAGACCGCGAAGTAAGGAAAGTGTGTAGTTTAACT
 AAGTGTGTTGTAATTTGAGAGTGTGGTGGGAGGTGGGGGAGACCGCGAAGTAAGGAAAGTGTGTAGTTTAACT
 TGGTGTCTTTGTAGAGTGTGGTGGGAGGTGGGGGAGACCGCGAAGTAAGGAAAGTGTGTAGTTTAACT
 CTTTGAAGCAAACTAAGCATTTAAAGAGAACTATTTTAAAGGTGTACACTTTTATTTTATTTCT
 CCAGAGAGGGTCTAATCTCATTTAGTGTGTCTATCGAAAGAACTTGAAGGCCAATCAAGCTGTTCGCTG
 GSCATTTGTATGGATTGACCTTCATTTGACACTCTCCAGCTGATTAAAGTTCAGAGTGTGATTGAGTT
 TTTGAAATATTATTAAGAAGAAAGCTTTTTCACATGACAAATGACACTCTCACACAGCTTTAGGCCCTAGTA
 GTTTTGTAGTTGACACAGGAGAGCAGTTTAAATGAGACCTTCTCTCTGCTACAGAAAGAAATAGGCAAT
 TGGTGTGAGCTGAGCTGAGCTGATATTATTAATTTAGTCTGAGACCTCTCCACCAATTCAGCGCTATACCTCCAG
 ACTAATTAATTTGAG
 TCTTCTGCAACTCAAAAGTAGAAGAGCGCCCAACTTTTCTCTGCGCTCAAGAGGCGAGACATTTGTGAT
 ATTTAGCATCAACAACACATTTATGATATATGTAAGTAATCGAGGGGCAATGCCACTTGTATTATCTCCCA
 AGTTTTCCAAGCAAGTACACAGACTCTGTTGATAGTTAGGGGCACTGTGTTTTCGGTCTATTTTGTAGTCA
 CTGTGACAGAGTTTGTATGCTTATCTGACATGCGCCAGTAGAGAGGCGATGATGGATGACATGAGAT
 GTGAGAGAGATCATCATCACTTCCCTCTCACAGAAATTAATCAAGAAGACAGAAATATATCTGTTTGG
 GAG
 GCTGATTTGGGTCTGCCATTCAGACATTCGAAATAAAGAGATACGTAATAATACCATTAATGAGTGTCT
 CTGAATATATTTGAGTAGGTTTGAATGCTCA

FIGURE 196

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNHICSVQGDFAQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAQFVFPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTLEHLEHNDLVKNFAHFPRLISLHSLCLRNRKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRILNSWKSLSIT
LAGNLWDCGRNVICALASWLSNFGQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG
HLLSAVTNRSDLGPPASSATTADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFTVTRRKQKQKQTMHQAAMSAQEYYVDYKPNH
IEGALVIINEYGSCCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTGCGAGCCAA
CTGGAGCCAGAACCAGACCCCGTGCGCCGGCGGCCGTTGAGTTCCCGGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGATTGCGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGACGATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTCTGGCGTCCCGCGCGGGCCGCTACGCTTCCACGGGCCGGCGCGCTGAGCGTG
GGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGAGGCGCAGCCGTG
GATCTGCGCGCCCTGCTCCAGCCCCT

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSIDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLPGASPVVRVRSISALGRTFTRDEDLAVFLASR
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEAQPWICAALLQP

[illegible]

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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIP
FARDAVKKCFVCLA

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FIGURE 201

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGCGTTCCTCCAGTCACCCCTCCGCGGTTACCCGCGGGCGCG
 CCGAGGGAGTCTCCTCCAGACCTCCCTCCCGTTGCTCCAACTAATACGAGTGAACGGATCGCTGGGAGGGT
 GGGACAGAAATTAGGGGGAGAAGGACAGAGAGCACTACCATCCATGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGCTTCATACCTTCTGCTGACCTGAGTCTTTC
 AACCACCTTTCTCTCCACTAGACCAGCAAAAGGTTCTACTAGTTCTTTTGTATGGATTCCGCTGGGATTACT
 TATATAAAGTTTCAACGCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAACGCAAGTTACTAATGTT
 TTTATTACAAAACTTACCCTAACCATTTATACTTTGGTAACCTGGCCTCTTTCGACGAGAATCATGGGATTGTGTC
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCCTGGATCACATGAATATTTATGATTCCAAGTTT
 GGGAGAAGCGACACCAATATGGATCACAAACAGAGGGGACGACATAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTCTTACTATTACATGCCTTACATGAGTCAGTTTCAITTTGAAGTAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAGAGCCCATAAATCTTGGTCTCTCTATTTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGCGCTGTCACTTCAGATATTGACAAGAAGTTA
 GGATATCTCATACAAATGCTGAAAAAGGCAAGTTGTGGAACACTCTGAACCTTAATCATCACAGTGATCATGG
 AATGACGCGAGTCTCTGAGGAAGGTTAATAGAATTTGACAGTACCTGGATAAAGACCACTATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGAGCTTCCAGAAAGGTGGCATTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTACAGAAATAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAGAAATTC
 TCAAAAGAAGCCATGAACCTCACAGATTTGTACCCTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATCTCCTCCTGGTAGTGTAAACAGCAGAAATAGCAAGAGGGGTATACCCCTTATTTATAGGGGTC
 TCTCTTGGCAGCATTTATAGTGATTGTAATTTTGTAAATTTTCAATTAAGCATTTAATTCACAGTCAAATACCTGC
 CTTCACAGATATGCATGCTGAATAGCTCAACCAATTTATCAAGCCTAATGTTACTTTGAAGTGGATTTGCATA
 TTTAAGTGGAGATTCCATAATTTGTCACTGTTAAAGGTTTCAAAATCTCGGGAACAGTTCGCAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGTGATACACACACACACACACATACACACACACCGACCAA
 ATACTACACCTGCAAAAGAAATAGAGTCTGAGAGTATGCTCCCATTTTCACTGTAGCATAGGGATAGATAAG
 ATCCCTGCTTTATTTGGACTTTGGCCAGATAATGTATATTTTAGCACTTTGCACTATGTAAAGTACCTTATAT
 ATTGCACTTTAAATTTCTCCTGATGGGTACTTTAAATTTGAAATGCACTTTATGGACAGTTATGCTTTATAAG
 TTGATTGAAATGACAACCTTTTGCACCATGTGCACGAATACTGTTACGCATTGTTCAAACTGAAGGAATTT
 TCTAATAATCCGAAATAATGACATAGAAATCTATCTCCATAAATGAGAGAGAGGAAGGTGATAAGTGTGA
 AAAATTAATGTGATAACCTTTGAACCTTGAAATTTGGAGATGTATTCACACAGCAGAAATGCAACTGTGGGCAT
 TTTCTGCTTATTTCTTTCCAGAGAACGTGGTTCATTATTTTCCCTCAAAGAGAGTCAAACTACTGACAG
 ATTCTCTATAATATTGTTCTGTCTATAAAATATTGTATTTCTGATGAGTCATATTACTGTGATTTTCA
 TAATAATGAAGACCATCATGATATCTTTCTTCTATATAGTTACGAATGGCCTGAATAGAAGCAACACGGA
 CCATCTCAGCAATGTTTCTCTGTGTTGAATTTTGCTCTTGAAATTAATCACTATTAATTACATTAA
 AAATCAAATGGATAAAAAAGAAAAAAGAAAAA

FIGURE 202

MTSKFILVSFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
ITNQRIGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
WEDPDDMGHHLGPDSPLMGPFVISIDIDKKGILYLIQMLKKAKLWNTLNLIIITSDHGMTQCSEER
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTAHPNLTVYKKEDVPERWHYKYN
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
IGVSLGSIIVVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTCTGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCCAG
 GACAGGCCCACCTTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCCTTGGCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTACAA
 CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCGCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTTGGCCCCGCACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCTGCTTGGTGGTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCACAAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCTGAGTTCCTTACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTATCCTGGACATGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAAGCGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACCTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
 AAAATCTATAAAGATATTCTGAAAAATGACAGAAATTTGACAAATAAAAGCATAAACGTGTA
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FIGURE 204

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNIN YKKWENEEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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GGGCTCGAGCTCGAGTGAATCGGCTCGAGGGGGCAGTGGAGCACCAGCAGGCCGCCAACAT
GCTCTGTGCTGTGCTCTGACCTGTGCGGCTGTCTGGGGGAAGCCGACAGCGAGTTCACGTACTTGA
AGTCGAAGGGGCTCCCTGCGGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTCTACCTCCCTCT
CAGGAATTTCTCCACTTCCGCCATGGGAAGCAGAAAAATTTGACAAGCTGGAGATAAGGACCT
TGATGGGCACTAGACTTTGAAGAATTTTGTCCATTTATCTCAAGATCATGAGAAGAAAGCTGA
GGCTGGTGTTTTAAAGATTTTGGACAAAAGAAGATGATGGACGCATTTGACGCCAGGAGATCATG
CAGTCCCTGCGGGGACTTGGGAGTCAAGATATCGAAGCAGGCGACGAAAAAATTTCTAAGAG
CATGGATAAAAAAGCGCAGCATGACCATGCACTGGAACGAGGTGGAGAGCATACCACCTCTCC
ACCCGCTGGGAAAAATCTCCCGAGATCACTCTACTGGGAAGCATTCACGATCTTTGATGTG
GGTGAGAATCTAACCGTCCCGATGAGTTACAGTGGAGGAGAGGACAGCGGGGATGTGTGTG
GAGACACTCTGGTGGCGAGGAGTGTGGGCGAGGGGCCGATTCAGAAAGCTGACCGCCGCCCTGG
ACGGCTCAAGGTGCTCATGGAGGTCCATGCCCTCCCGCAGACAACATGGGCATCTGTGGT
TTGTTTACTCAGATGATTTGAGAAGGGGGCCAGGTCACCTCTGGCGGGGCAATGGCATCAA
GTTGTTTCAAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
TTGTGTTGTGATGACCAAGGAGACTTGTAGGATTCACAGAGAGCTTTGTGCGAGGGTCTTGCA
GGGCGATCGCCGAGACAGCATCTACCCATGGAGTCTCTGAAGACCCGATGGCGCTCGC
GAGAGCAAGCGAGTACTGACGAATGCTGGATCGCGCAGGAGGACTCTGGCCAGAGAGGGGG
TGGCGGCTCTTCAAGAGGATGTGTCCCAACATCTGCTGGGATCATCCCTATGCGCGCAT
GACCTTGCAGTCTAGAGAGCTCAAGAATGCTTGGTGCAGCACTATGCGCTGAACAGCGC
GACCCCTGCGGCTTTGTCTCTGGGCTGTGGCTGTGCGCACCTGCTCAGTACTTGTGGCCAGTGG
CGAGTACACCCCTGGGCTAGTTCAGAGCCGCGGCTGGCGAAGGCTCTATTGGAGGCGCT
CCGAGGTTGACCATGAGCAGCCTCTCAAAACATATCTCGGAGCAGGGGGGCTCTGGGCT
GTACAGGGGGCTGGCCCAACTTCATGAAAGTCACTCCAGAGCTGAGCATCAGCTACGTGTG
TCTACGAGAACTGAAGATCACCTCGGGCTGCACTCGCGGCTGAGCGGGGAGGGGCGCCGCT
GCAGTGAATCTGCTGATCTCTGGGGCGCAGGCTCGGGGTGTGACGCATCTCATTTCTGTGAATG
TCCCAAGCTCAAGCTGTCTCGAGCGCAAGCTGTGAAAAACCAGACGACCCGAGAGGGGG
GGGAGGCGTGGCGAGCCGCAAGCTGTCTGCTGCTGAGCCGAGAGCGCTCTGTTGTTGTT
GGGAGGAGGAGGATTTCTGGGCGAGGCTGAGCGAGGGTGGCTCTCATCTGTGATGAA
GGAGAGGACATTTTCTGCAGTCTGCTCAAGTGTGAGGCGAGGCTGAGGCGGCTTACT
TCTTCCATTTACGCTCTGCAGGCATCTGTGGTGTGAGGCGGCGGCTCTGCTCTGCTCCG
ATCTCCCTTGCCTCTTGTCTGCTGCTCTGCTCTGAGTGAAGGTGGGAAGAGGCTCAG
CCCACTCCCAACCCCTCTGCTCAATCCCAATATCATGATGAAAGTGAAGTCACTGTGGCT
CCAGGCGCTACTTCCCAACTCAGACATTTAGCCGCAACTTGGCTGTGAAGGAAGGAAGA
GATCTGGCTTTGGTCACTGTCATCTGAGCCCTGCTGATGCTGGGCTCTCGGCACTGCT
TGGAGTCTCAGGGGGCTCGGGCTGCTTGGCTGGCTGCACAGAGGCAAGTCTGGGGCTCA
TGGTGCTCTGAGCTGGCTGGACCTCTGACAGATGGGCCCACTCAGAAGCAAACTCACTG
TCCCACTGTGGCATGAGGCAAGGCACTGAGCACCATTGTTGAGGCGCAAGGCGAGCGTTTGT
GTGTTCTGGGGGAGGAAGGAAGAAGTGTGTGAGGCTTTAAATTTAGACTGTTTGGAAAAGGG
TTTTTCTCAGAAAGGACAGCGGCAAAATGAGCGACTTTGTGCTCTCAGAGGAAGACAGG
GAGCAGGAGTGTGGCTGACTGCTCAGATGTGTTCTGAGCGCTGGGGGTTTCTGTCCAAC
CCAGCAGGGGCGCAGCGGGACAGGCCCACTTCACTTGTGTGTCACGCTTGGAACTATTT
ATTTGTGATTTTGAAGCAGGATTTGCTCTAATATTTTATGTATGTTTGAATTTTAAATTA
GCTTGCTCATTTTCAAGTATTTGAGTTTATGATTTATGTTTGTGTTGATGTACCTTCCC
AAGCCCGCCAGTGGGATGGAGGAGGAGAGAGGGGGGCTTGGCCGCTGCACTCAGAT
CTGTCTCAGAGAAATTTCTTTGGGACTGGAGCGAGAAAGCGCCAGAGGACAGCGCTCT
GCTCTTTTCTTTTGGCAGGTTTGGGGAAGGGCTTCCCCAGGCTTAGGATTTAGGTTTGA
CTGGGGGGCTGGGAGAGAGAGGAGGAACCTCAATTAACCTTGAAGTGGAACTCAGGTTATTT
CTGCGCTCGGAGGGTTTCTTTTACTCTTTTCTGAAATCAAGGCACTGAGGTGCGCTCT
CAGTGTGAAATTTGGTGGGCGGGGCTGGAGGAGAGGGTGGGGGCTGGCTCGCTCCCTCC
GACGCTTCTGCTGCCCTTGCTTCAAAATGCGCGGCAACTGGGCACTCAGGTTGCACTTCC
ATTTCCACCAAGATGACCTGATGAGGAAATCTCAATAGGATGAAGATCAATGCAAAATTT
GTTATATATGAACTATAAATGAGGTCGTCAAAAGCAAAATGAAGAAGAAATGGAGCTTAG
AAGTTGTCAATTTAAAGCAGCCTTCTATAAGTTGTTTCAAAGCTGAAAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 206

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRKVLQMQVHASRSNNMGIVGGFTQMIREGGARSLWRNGI
 NVLKIAPESAIFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIQSSIIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPMMLGIIIPYAGIDLAVYETLKNWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

[illegible]

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FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLL
LNQCGSLYYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS
RHTCVSSFPEPISPEWVRTRPFPILPFPPLQLFCFLVAIRVPFPWTVVRKTEAGVWD



FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACC**ATGA**AGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTTGCAGCTGTAGAATCTCTGAGCTGCCGTGCAGTGTAA
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTCTGTGGGAAGCCCTGGAAATGCTATGAAGAAGACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGTCTGAAAGGCTGTT
 CAACGTGAGTAACGCCACCTGTGAGTTCTGTCTGGTGAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAATGTAACAGCTTAACCCCCACGTCTGCACCAACCACT
 TCCCACAACGTGGGCTCCAAGGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCC**TGA**GGTCTGGGGCTGCACTTTGCCAGCAGCCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCAGCCCTGCGGTGCTGACACCTCTTTCCCTGCTCTGCCCCGTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTCTTCTTATTATTA
 AAGCACTGGTTCATTCAGTCCAAAAA

MKGILVAGITAVLVAAVESLSVCVQCSWEKSCVNSIASECPHANTSCISSASSSLETQV
 LYQNMFCSAENCSEETHITAFTHVHSAEEHFHFVSQCQCKECSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGPWKCYEEQCVFLVAELKNDIESKSLVLKGCNSVSNATCQFLSGENK
 TLGGVIFRKFECAVNSLTPTSPAPTSNNGSKASLYLLALASLLRGLLP



FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTCACTGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCC**CATG**GTCCTCCCGCCGCCG
GCGCCTGTCTGGGTCTGTCTGAATCTGGGTCCCCGGCGCGGGGGGCCAAGGCCTG
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG
CTACCGGAGCACCGCCCGACTGGTCTTCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCCTACCCACAG
CCATGCCATCTCCTGAGGATCTGCGGTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAGCCTTGCACTATCAACAATGTC
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTAGTACAGAAAAACAACTGGAAAA
CACAA

MVPAAGALLWVLLNNGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
 ILEDENDAMADADRLAGPAAEELLAATVSTGFSRSSAINEDGSSSEGVVINGAKDSTSRRL
 PSATPNTAGSSSTRFIANSQEPEIRLTSSLPFRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
 SPSPATAMPSPEDLRVLMPWGPWHCHCKSQSTMRSRSGKLHGLSGRLRVGALSQLRTEHKPC
 TYQQCFPCNRLRECEPLDTSCTDNCAQSSTSTRTTTTFPFTIHLRSSPSLPAFCPCALA
 FKKVRVIGLEDIWNLSLSSVFTMPOSDIDRNR

FIGURE 215

CCGGGTCGACCCACGCGTCGCGGGGAGAAAGGATGGCGCGCCTGGCGCGCGGTGTGGTCTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCGAGGGCGACCGCTGAGCCGSGTGACCCGCACTGCGTACTGCAGTGGCAAGAGCA
 GAACCTGCTCTGGGGGCGCTCTGAATCACTTCGCGTCCGCGCAGCCAATCTACATGAGCTAGCAGGCTGGACCT
 GTCCGGACGACTGTAAAGTATGAGTGATGTGGGTACCCGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCCT
 CAAGTCCATGGCAAGTGGCCCTCTCTCCGCGTTCTCTGTTCTTTCAAGAGCGCGGCATCGGCCGTGGCCCTGCTTTCT
 CAATTGGCTGGCCAGCCTGGTGATGCTCTGCGCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCCATGTACACACA
 CCTGTGTGGCCTTCGCGTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCTCCACTGTATCCTACACTCAATCTACCTGTGCTGGCTCAGGAC
 CGTGGGGCTCGACAGCCAGCTGTGGTCAGTGCTTCGCGGCTCTCCTGCTGCTCATGCTGACCGTGCACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCTGTGGAACAGCAGCGCGCTGCCTCAGCTGCGCAAGTGGCTGGTGGTGGTCTT
 GCTGCTGACGGGGCTGTCCCTGCTCGAGCTGCTTGACTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGCACATCAGCAACCTCCCTGTCCAGCTCCTCTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACTGAAGACCTTGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC
 GCCCTGCTGGCCTCCCTCTCCCTCAACCTTGAGATGATTTCTCTTTCAACTCTTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCGAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGCGAGCCCTCTACCTCCTGGAGCTGAACCTGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCTGTTCTCCTCCACAGCCTCCTCCACATCCCGAGCTG
 CTTGGCTGGTCTGAAAGCCTCTGTCTACCTGGGAGACCAGGGACCAAGGCTTAGGGATACAGGGGGTCCC
 CTCTGTATACACCCCCCACCCTCCTCCAGGACACCACTAGGTGGTCTGGATGCTTGTGTTTGGCCAGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTCCCTGCGAGGTTCCAGGAGGCCCTACCATACTCCCTTTCAAGGCCAGGGCTCCAGCAAGCCGGGTGTGTG
 AGGATCCTGTGCTGCTGCTGGTTGAGAGCCTGCCACCGTGTGTCGGGAGTGTGGGCGAGGCTGAGTGCAATGG
 TGACAGGGCGTGAAGCTGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCATGTGGAGACGGGTGTGTG
 CGGGGAAGAGTCTGGCTCTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTTAGCCTGGGTAGGGGAACGTGTG
 TGCGCGTCTGTGGGCATGTGAGATGACTGAGTCCCGTGAATGTGCCACAGTTGAGAGTTGGAGCAGAGT
 GAGGGAAATCTGTACCATCAATAACTTGTGAGCGGCCAGCTCTGCCAAGACGCCACCTGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCTGTGTGATGTTCCCTGTCTGGTGCCCTTTGCCCGCCTCCTGCAAC
 CTCACAGGCTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTCGGAGGACAGAGGAAGGAAATGGGGATGGC
 TGGGGCTCTCTCCATCTCTCTTTTCTCCTTGCCCTTGCATGGCTGGCCTTCCCTCCAAAACCTCCATTCCTCT
 GCTGCCAGCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGGCGATTTGAGGGAGAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTCTCTCCCTTCCAGAGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCGAGGGCC
 ACACATATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACAGCAGCCCTGGCATGTTCTGCCCCACAGG
 AATAGAAATGGAGGAGCTCCAGAACTTTCCATCCCAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGACTCGGTG
 GCTCGCTAGCTCTTTTGATACTGAAAACCTTTTAAAGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA
 TTTCCAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAWFSTVFHTRDSDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSFAFRALLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

GGCCGCGCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCTGTA
CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGGCAAA
ACTCCAATATGAGGACAAGTTCGCAAAATAATTTGAAAGGCCAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTCATAGTTCCAGCTCCAGTTTGAAGAGAAGATGATGCTGCCTC
TTTGATCTTGAATATTATGTTCATCATAGATGGACAATGCGCAGAGACCTGCTTTCCTTGGTGG
TCTTCAAGTGGTGATCAATGGGCTGAAACGACACAGAGCCCTCGTGAAGGAGTATGTCGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA
GCCCTGCGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCGCTCACTGCAAGAAGAAGGT
CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCTGAAGC
TCGGGGGGCTGCAAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCCGAGGAGGAGGCTGA
GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG
GCCTGTGGGAACAGGGGTGGTGCGAGATCACGGCCCCACCTCCTGGCGCTGCCCGAGCATGAT
GCCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCACGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
TGGCCATTTAAATGGAACACTGAAGGCCAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 218

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQMDNAQDLLSFGGLQVVINGLNSTEPVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTVEVLAVRVVITLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLALLPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTCATTGGGGTTTCGGTTCCTCCCTTCCCTCCCTCCCGGGGTTCGGGGTGCATTTGACACCGGCCCTCGTGGGGTTCGCGTTGCCACCCCA
CGCGGACCTCCCAAGTGGCGGCCCTCCATTTCCTGTCTGGTTCAGGCCACACCCCTC
TTCCACCTTGACACGCGATGGGGCTGCGGTGTTTTTCGGCTGCATCTTTCGTTCGCTTCGGC
CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGAGCCCGCTTCGGTTATCATCTCGGTG
CGAGGGGACATTTTTCGGCTGCTCTCCCTGCTCTGGCCTCTGTGCTCGGTTTCATCTCTGG
TCCATTGTACCGACCGGCTCAGATCGCCCGCTCCAGTACGGCCTCTGATCTTTTTTGGTGTCTGG
GCTCTGTCTCTTACAGGAGGTGTTCCGCTTTGCCATCTACAAGCTGCTTAAGAGGACAGA
TGAAGGGTTAGCATTCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCGACAGTGGCCT
ATGTTTCTCGTCTCTCTTCCTGGTATCATGATGGTGTCTTCTCTGTATCAATATTTTTGGCT
GATGACATTGTGGCGAGTGTGGTGGGATCATGAGACTACCCCTATTACTTCTGACTTC
AGCCTTTCTGACAGCAGCCATTATCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
CCTGTGAGAGGACAGCGTATCTGGGCTTTGGGCGTTGGTGGTGGGAGTCACTCATGACATCTG
GGACTGACATTCTGACACCTCGTATGAGGCGACCGCTGCTGCCCATCTATGCACTCACTGT
TTCCATGGGGCTTCGGGCTTGCATACAGCTGAGGGGTCCCTCCGAGATATTACGCGCAGCC
TCTTGTGTAAAGGACTGACTACCTGCAGCTGATCGCCTGACAGATCCCACTGCCTGCTCACT
CCCATGACTGAGGCCAGCCACGCCCGGGTCCATTGCCACATCTCTGCTCTCTTCTGCTGCT
GGTCTACCCCACTACCTCTCAGGGTTTTCGTTTGGCTTTGTGACCTTTAGCTGCTTAAGTCT
TACAGGAGCGAGCTGGGTTCAGCCAGTCACTGATGCTGGTGGTGTGAATCTGCATCTATCCC
CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCGCCCTGTGTCACTGCTCTGCTCTCAC
CTGTGCAAAAGACTACCTCCTTCCCTCTGCGAGCGACGCGAGGAGGACCTGGGTGAT
GGTGATTTCTGCTCTGCGCATCCACCCGAGACTGAGGAACTGAGGAGGAGCCCTGGGCT
CTGGGCTGCCCTCTGATGCTCTGCGCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
GTGGCAAGAAAAGGACCTAGTTTATGCCATTTGCCCTGGAGATGAATTAATGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTATCCCTCAAGACTGCACATCTTGGTCTTTTCTCT
AGGCTCAGGGGGAGAACATTTTGTGTGATAAATACCTAACTGCTCTTTTCTTTTCTTTT
GAGGTGGGGGGAGGAGGAGGTATATTTGAACTCTTCAACCTGCTTGGGCTATATTTCTCT
TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCTTGGTCCCGACCTT
GGGGGAGGAGGAAGGAGTGCATGTTTGGGAAGTGCATTTGCTGGAATCAATGTTTAACTCT
CCTTAACCAACGACTCCTCTCTCCCAAGGTGAAGTGAGGGGTGCTGTGGTGAGCTGGC
CACTCCAGAGCTCGAGTGCCACTGGAGGAGTCAAGTACCATCACTCGTAGGAGGAGGGG
GAGATTTTTTTGTAGTTTTTAATTTGGGGTGTGGAGGGGGGAGGTTTTCTATAAATGCT
ATCATTTTCTGCTGAGGGTGGAGTGTCCATCTCTTTAATCAAGGTGATTGTGATTTTGAAT
ATAAATAAAGAAATTTGTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
 SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS
 FGIISGVFSVINILADALGPGVVGIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
 YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLLCKD

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FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGCTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCTTCTGATTTTTGGTGCCTGCTGNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNCTGAGTGAGGACGGAAGATCACCATTTCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCTATTAATTCCTGAATTAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTTCCACNTG
ACCAGCCATGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTCGCGTTCGGCCCCGCCCTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGCC
TTCTACAGGAGGTGTTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAAGAAAGTGGCCGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTCGTGCGGTTGCGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGCCCGT
 CTTGTGGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCCATGGGCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACACCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTACCAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCCTGGCCACTCT
 AACGACCTCATGCTCATAACTGAACAGAAGAAATTCGTCCCACTAAAGATGTCAGACCCAT
 CAACGTCTCCTCTCATTTGCTCCCTCTGCTGGGACAAAGTGCTTGGTGCTGGCTGGGGACAA
 CCAAGAGCCCCCAAGTGCACTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCGCTGTGGCTGCAATGGCTCCC
 TGCAGGACTCGTGTCTTGGGGAGATTACCCTTGTCGCCGCGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCTTGAGTCTAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCGAGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTATCTCTCCAGCCCCGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGGTTCGCTCTAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA
 CTGAGAAGTGGAATAAAAAA

FIGURE 226

MATARPPWMVLCALITALLGVTEHVLANNNDVSCDHPSNTVPSGSNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRI RPTKDVRP INVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGR DSCQGD SGGP
VVCNGSLQGLVSWGDYPCARP NRPGVYTNLCKFTKWIQETIQANS

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FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATTGGCGGGCGTGCCCAACTT**GAGGACCGGCCGCGCGCA**
CAAGCCGACGCGGCGAGCTGCGGGTACGCTGCTGTGCACCGCTGCTGCTGGCCCTTGGCTGTGC
TGCTGGCTGTAGCTGTCACCGGTGGCGTGTCTT**CCTGAACCACGCCCCACGCGCCGGGACCG**
GCCGCCCACTGTCT**CAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA**
AAGGCGCGACAGCTCGCACTCAGCATCCTCATTGACCCGCGCTGCCCCGACCT**CACCGGACA**
GCTTCGCACGCTGGAGAGCGCCAGGCTCGGTGCTGCAGGCGCTGCACAGAGCACCAAGGCC
CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAAGCTGCC
CGGCTGCTGCGCCGAGCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG
GCTGCTGGGCGAGGGCTCAGCGCCTGCAGAGTGAGCAGGGGCCCTCATCCAGCTTCTC
TCTGAGAGCAAGGGCCATGGCTCACCTGGTGAACTCCGT**CAGCGACATCCCTGGATGCCCT**
GCAGAGGACCGGGCGCTGGGCGGGCCCGCAACAAGGCGACCT**TCAGAGAGCGCTGCC**
GGGAAACCGCGCGCGGGCTGTGCCACTGGCTCCGCGCCCGAGACTGCTCGGACGTCCTC
CTAAGCGGACAGCAGGAGGATGGCGTCTACTCTGTCTTCCACCCACTACCCGGCGGGCTT
CCAGGTGTACTGTGACATGCGCACGACGGCGGGCGGTGGACGGTGT**TT**CAGCGCCGGGAGG
ACGGCTCCGCTGACTTCTCTTCGGGGCTGGGACGCGTACCCGAGACGGCTTTGGCAGGCTACCC
CGCGAGCACTGGCTAGGGCTCAGAGGATCCAGCCGCTGACCAACACAGGCTGCC**TACGAGCT**
GCACGTGCACCTGGAGGACTTTGAGAATGCGACGGCTATGCCCGCTACGGGAGCTTCGGCG
TGGGCTTGTTCTCGCTGACCTGAGGAAGACGGGTACCCGCTCAGCGTGGCTGACTATTCC
GGCACTCAGCGACTCCCTCTGAAGCACAGCGGCATGAGGT**TACCA**CCAAAGGACCGGTGA
CAGCGACCACTCAGAGAACACTGTGCCGCTTCTACCGCGGTGCCTGGTGGTACCGCAACT
GCCACAGCTCCAACTCAATGGCGAGTACCTGCGCGGTGCGCACGCTCCTATAGCGACGGC
GTGGAGTGGTCTCTTGACCGGCTGGCAGTACTCAAGTTCTCAGATGGCAATTCG
CGGGTCCGGGAGGACCGCTAGACTGGTGCACCTTGTCCTTGGCCCTGCTGGTCCCTTGCG
CCATCCCCGACCGACTCACTCTTTCTGTAATGTTCTCCACCCACTGTGCTGCTGGCGGAC
CCACTCTCCAGTAGGGAGGGCGCGGGCCATCCCTGCACGAAAGCTCCCTGGGCGGGTGAAGT
CACACATCGCTCTCGCGTCCCACCCTCCATTTGGCAGCTCACTGATCTCTTGCCCTC
TGCTGATGGGGCTGGCAAACTTGACGACCCCACTCTGCTTGGCCCCACTGTGACTCCGG
TGCTGTTTGCCGCTCCCTTGGCAGGATGGTGGAGTCTGCCCCAGGCACCTCTGCCCTGCC
CCCAAAATACCCGCAATFATGGGACAGAGAGCAGGGGGCAGACAGCACCCCTGGAGTCCCTC
CTAGCAGATCGTGGGAATGTCAGGCTCTCTGAGGTCAAGGTCTGAGGCGAGTATCTCCAG
CCCTCCCAATGCCAACCCCACTGGTTTCTGGTGGCCAGAGAACCCACTCTCCCCAA
GGGCTCAGCTTGCTGGTGGGTGGTGGCCCCATCTACCAAGGCTGAGGTCAAGGTCAAGGT
GAGCTGCTGCTTTGGGGACCCACGCTCCAGGCTGAGACAGTCTCCCTGGAGGCCACCCAC
CTGTGCCCCGGCAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCCACTGCTCTG
CTCTAAATAGGCCCAACCACTCCCAACCAAGCTCCGCGCGCTCTCTACCTGGGGCAGC
CGGGCTGCCATCCCAATTTCTCTGCTCTTGAAAGGTGGGGGGCTGCACCGTGGGGCT
GGACTGCGCTAATGGAAAGCTTTGGTTTCTGGGCTGGGGCTAGGCAGGCTGGGATGAG
GCTTGTACAACCCCAACCAATTTCCCAAGGACTCCAGGCTCTTGAGGCTTCCAGAGG
GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGACAGGCTGGAGCCGG
ATTGACCGTGGCCACTGCACCGAGGCCAGGCCCGGCCGGCGAGTGGTCAAGGACAGGGA
CCACCTCACGGGCAATFATGGGTGGGGGAGCTGGGGCACAGACAGGCACCACTTGAACA
CTTTCTGTTGTAATCTCCCAACCCAGCACGCTGTCTATCCCACTCTTGTGTGCACACA
TGCAGGGTGAGACCGCGAGGCTCCAGGACAGCACGCAAGGCGAGGCTGGAGCCGG
TCCTCAGCTGTCTGCTCAGGACCTTGAGCCCGCTGCGTTACGTGAGGCCAGATGCAGG
CGGCTTTTCAAGGCTCTGATGGGGGCTCCGAAAGGCTGGAGTCAGCTTGGGAGCT
GCTAGCAGCTCTCTCTGGGAGGAGGGGAGGTGGTCTCTCCAAAGGACACCCGATGGCA
GGTGCCTAGGGGTGGGGTTCCGTTCTCCCTCCCACTGAAGTTTGTGCTTAA
AACAATAAATTTGACTTGGCACCACTGGGGGTTGGTGGGAGAGGCCGTGTGACCTGGCTCTC
TGTCCAGTGCCACCAAGGTCACTCCACATGCGCAG

FIGURE 228

MVNDRWKTMGGAAQLEDRPRDKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDAQEQLLDTLADQLPRLRARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFFRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSSLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
VEWSSWTGWQYSLKFSEMKIRPVREDR

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FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTCTGAAGTACTGCTACAGTAGCCCGCGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCAGGAGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC
 TTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCTCTCAGAGTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGCGCCCTGACAGTGGCAAGGCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAAGT
 TTCCATATTATAATAGATGTCAACAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGAATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCTGTG
 TTTCTGTCTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCTAT
 GTCTTCTTACACTTGGTGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTCTTTTTGTTTGTTCAGTTTCATACTAGTCCCTTCCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCGGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTCTGTGCCATTAAGACTCTGATAATTG
 TCTCCCTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNICYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAAGGAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACCTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC



FIGURE 232

GCCGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTTCGGCTCGGGGCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGGCCCGCGGGG
 CCCGAGCCCTTCGGGATCCGCCCCCTCCCCGGTCCCGCCCCCTCGGAGACTTCCTTGGCTGCT
 CTGGGGGTTTCGCGGGGCCGGGACCCGCGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG
 TCGGTTGCTCGGGCCCGCAGGGCCCTGCGCCGTGGGCATCTCCCTGGGCTTCACCCTGAGCCT
 GCTCAGCGTCACTTGGGTGGAGGAGCGCTGCGGCCGAGGCCCGCCCAACTGGAGACTCTG
 AGTCCGCGCGCGCGCAACACCAACGCGGCGCGCGGCCCAACTCGGTGCAGCCCGGAGCG
 GAGCGCGAAGACCCCGGGCGCGCGAAGCGCCGCGGAGAATTGGAGACCGCGCTTGTGCC
 CTACCACCTGCACAGCCCGGCGAGGCCGCAAAAAGGCCGTGAGGACCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGAGAGGCTGCTGCTGGCGGTGCTGACCTCTCAGACACCGTGCC
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCTGAC
 GGGCGCACGGGGCGCGCGGGCCCACTGGCATGGCAGTGGTGACGCTGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTCG
 TGGTCTCTCTGGTGCTGACACCACTACACCGAGGCGCACGGCTGGCACGCTTAACCTGG
 CCACCTCAGCTGGCTCCGCGGCCCACTGTACCTGGGCGGGCCAGGACTTCATCGCGG
 GAGAGCCACCCCGCGCTACTGCCACGGAGCTTTGGGGTGCTGCTGCGCGCATGCTG
 CTGCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGGCGCCCTGA
 CGATGGCTGGGTGCTGCATTTCTCGATGCCACCGGGTGGGCTGCAGTGGTACCCAGAG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGCAGGAGGGGGACCTCAT
 TTCCGAAGTGGCTGACAGCCCACTGTGCGTGACCTGTGCACATGTACAGCTGCACAA
 AGCTTTGCGCCGAGCTGAAGTGAACGACGATCCAGGAGATCCAGGAGTTACAGTGGGAGA
 TCCAGAAATACCGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGAGTAT
 CCAGCACCATCCCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCGCATGGCTCACCCGCTGCCACTGCGTGGGCTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCCTACCACCCGGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGATGGCTACCGACGCTTTGATCCGGCCGGGGTATGGA
 ATACACGCTGGAGCTGCAGCTGGAGGCACTGACCCCCAGGGAGGCCCGCGGCCCTCACT
 GCCGAGTGCAGCTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCTGTGCCCTATGTCACT
 GAGGCCCTCACGTCTCACTGTGCTGCTGCCCTTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG
 CTCTCTGGAGGCCCTTGGCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCATGCAGATGCTTTCGCACT
 GTCAAGGCCCACTGGCAGAGCTGGAGCGCGCTTTCCCGGTGCGCGGCTGCCATGGCTCAG
 TGTGACAGACGCCCACTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCTGGATGTGTACAGCT
 TGGACACACTGTTCTGCTGGCCGGGCCAGACACGGTGTCTACGCTGACTTCTCTGAACCCG
 TGCCGCACTGCATGCATCTCCGGCTGGCAGGCCCTCTTTCCCATGCATTTCAAGCCTTCCA
 CCCAGGTGTGGCCCCCACCACAAGGGCTGGGCCCCAGAGCTGGGCGGTGACACTGGCCGCT
 TTGATCGCCAGGCAGCCAGCGAGGCCCTGCTTCTACAACCTCCGACTACGTGGCAGCCGCTGGG
 CGCTGGCGCAGCTCAGAACAAAGAAGAGGAGCTGCTGGAGAGCTGGATGTGTACAGCT
 GTTCTTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT
 ACCGGGCTGACGTCAGCGAGGCTCAGTGAGGACCTGTACCAACCGCTGCCCTCAGAGC
 GTGCTTGAAGGCGCTCGGCTGCCGAACCCAGCTGCCCATGCTACTCTTTGAACAGGAGCGAGG
 CAACAGCCT**TGA**CCCCACCTGTCCCCGTGGGCGCTGGCATGGCCACCCCACTT
 CTCCCCAAAACCAGAGCCACTGCCAGCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCCC
 AAGCTGGCCCACTGGTCCCTCTCTGGCTCTGGGGTCCCTGGGCTGTGCACAGCAGCTGGG
 GGACGTGCCCCAGGACCACTTCTCATCCCAAAACCCAGTTTCCCTGCCCCCTGACGCT
 GCTGATTGGGGCTGTGGCCTCCACGTATTTATGCAGTACAGTGTGCTGACGCCAGCCCTGC
 TCTGGGCCCTGGGGGCTGGGCTGTAGAAGAGTTGTTGGGGAGGAGGAGCTGAGGAGGGG
 GCATCTCCAACTTCTCCCTTTTGAGACCTGCCGAGCTCCCTGCCTTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGFVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKAVRTRYISTELGIRQLLVAVL
TSQTTLPFTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFDWFFLVPDTTYTEAHLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELEPTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVIGTALEELN
RRYHPALRLKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTV
TPDFLNRCRMHAISGWQAFFPMHFQAFHFGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTQLAMLLFEQEQQNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCGCTTTTGTAGAAGCTTGATTTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAAGCTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACTGGAGGCAAAG
 AGGGTTGCTCAACGCCCGCCTCATTGGAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT
 TTCCCCGCCCCCTGAGACCCTGCAGCACCATCTGTCT**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCAGCGGCACGCGAGGGCTCCCGCCGCCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAACTTGATGAGAAGAACCCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGCAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**CTG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 235

MAAGLFGLSARRLAAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFVGSIIILVLGSTFVAYLPDYRMKEWSRREAER
LVKYREANGLPIMESNCFDPSKIQLPEDE



FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAAGCGGCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG



FIGURE 237

GCGGGCGCT**TATG**CCGCTTGCTCTGCTCGTCTGTTGCTCTCTGGGGCCCGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTGCATACCCCCGCTGCCCTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCCGCACGCGCTGGGATTCCGGAGCTTCAGCGGGAAGGAGTG
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATCACACAAGGCTTTTGGAGACCCGATACTGGGGGCCACCCCTTCTGTC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTCCAAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCCTCAAACCCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCCACACAGCTACCACTCCCAAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTGATGCCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAAACCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGAGCTCATCTTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCAGTGCCTTCTCTGC
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACACCCACCCATACCGGGCCCTTCCGGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGGG
 GCTGTATGTGCACACCCCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC
 ACTACCAGCTGCCCAGGACCGGCTGCAACCCACCTTCCTGGAGATGCTGATTCACTGCGG
 GCCAATCAGTACCAAGGTTTCCATCCAGTTTGGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CAGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCTGTTCCTCA
 GTCTCTGATGGCTTAACTACTTTGTGCGGCTCTACACGGAGCGCGTGTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTACAAATCTCCTCACCCGAACCTTCCACATCAGGAGCCCCGCACAGGT
 GGCTTGCCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCT**TA**GATT
 CTTGCCCTTTCCAGCAGTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGGC
 CTACAGCTGTGTTGTCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTA
 CTTAGAAATTCATTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGCTCGGTGGCTGATTGTGGACGACAGAAAAAGATTTCCATCACCACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAATAAAACGGCTGTTCCGTGAAAAA

FIGURE 238

MPLALLVLLLLPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
 RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWK
 ELSNVLSGIFCASLNFIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
 KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCNRARCTISISWELRQTL SVVFD AFITG
 QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTYQDVILGTRKT
 YAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
 PYRAFPVLLLDTPVWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
 VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPMSVAAKPV DWEESPLFNSLFPVSD
 GSNYFVRLYTEPLLVNLPDPFSMPYNVICLTCTVVAVCYGSFYNNLLTRTFHIEEPRTGGLA
 KRLANLIRRARGVPPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAACTGGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCGTAGCCAGGATGGGAGGCCAAGTGTCAGGC
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCCCTTCTACCTCTGGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGTCTCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCAA

FIGURE 240

MGSSSFVLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63



FIGURE 241

AAACCTCAGCACTTGCCGGAGTGCTCATTGTTAAGACAAAGGGTGTGCACTTCTTGCCAGG
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCAGCCACCCACCC**ATG**AGGTCCTGCCTGTGGAGATGCAGGACCTGAGGCCAAGG
 CGTCCAGTGGCTCCTTGCTTCTGGCTGTCTGGTCTTCTCTCTCGCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAACAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTTAAGTCCCAGGACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACCCAGGCACCGCCGAGGAGGAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAACCATGGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGACACAAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTGAGAGAAGCACCCAGGGCAAAGCGGCAACCAAGCCAAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCCACCTTAAGGAGAAGAAACCTCAGGCCACCCACCCCTTGCCCTTTCCAG
 AGCCCCACGACCGCAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGGCTTCAGACGACTTGCCTTGACTCTG
 TGAAGATCAAAGCTCCAAGTCGCTGTGGCTCCAGAACTCTTTTGCCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCTTGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAAGTCTGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCTGCTGCTTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGATCACTCTGT
 GCCGTGGTGGGCAACGGGGCATCTGAACAACTCCACATGGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTACC GCCTTCCCTGACCCAGTCACTCCTTATATGGGCAAT
 CGGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCTTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCCGGGAAGCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGA
 TGGTGCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGCTCGGTG
 CCGGAATCGCCAAAGCCAAAGAACT**GCA**CGGGGGCCAGGGCTGCCATGGTCTCCTTGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAAATTGAGGTCTGAAGTCTCTCAGTACATTGCTGTAGGTCTTGAGGCCAGG
 GATTTTTTAATTAAATGGGGTGATGGGTGGCCAAATACCACAATTCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTCTACTAC
 AGATTGTCTAGAAGACCTTCTAGAGTTATCTGATCTAGAAGGTCTATACTTGTCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACTGATAATAATACAAATGATTGTT
 GTCATGGAAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSClWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNGGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVT TAVI PPKEKKPQATPPPAPFQSPPTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVT RFPVPVQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFTAFSLTQSLLLILGNRGFKNVP
 LGKDVRYLHFLEGRDYEWLEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLHHPDFL
 RYMKNRFLRSKTL DGAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFS DHYYDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTGTTCCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTTGCAGACAGACTCTTCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATT



FIGURE 244

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRLYHNT
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

[illegible]

FIGURE 245

GGGCTGGGCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCTCGGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCGCGCCAGCCCCACCATGCGCCACCGGGGGCTCCGCGGGGCCGCGCG
 CTCACCGCAATCGCTCTGTTGGTGTCTGGGGCTCCCTGGTGTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCTGCAGTCTCTCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAAGTAGA
 ACTATGAGGGGTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGT
 TCCGTGAGCAGCTGGCAGTAGCCCTCCTCTCTGCGTGGCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
YMPPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

GGGGAGC TAGGCCGGCAGTGGTGGTGGGCGGCCAAGGGTAGGGTGGCCCAAG
 CCCCAGTTAGGTAGAGCAAGAGAGTGTGTTTCTGCCCTCAATGGTCCCTGCACCAATG
 TCTATTCTACTTTCTCACTGTGGCTCTTCTAACTGTGTCACTCTCTATGGTGTACAG
 CACTGAAGCACTTCCAAACGTGTAGTATGGGACCAATTTCTTGGATAAAATACGACTGT
 CTAGTAGCTCATCCCACTTCTATTATGATCTCTGTATCCATGCAAACTTACACGCTGAC
 TTTCTGGGGAACCAAGATAGAAATCACAGCCAGTCAGCCACCACGACCATCATCTGTGA
 TAGTCAACCTTCAGATATCTAGGGCCACCTCAGGAAGGAGCTGGAGAGAGCTATTCGG
 AAGAACCCTCGAGTCTCGGAACACCCCTCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCCTCTTGTGGGCTCCCGTACACAGTGTGATTTCACTATGCTGGCAATTTCTGGAGA
 TTTCCACGGATTTTACAAAGCACCTCACAGAACCAAGGAAGGGGAATGAGATATGACAC
 CAACACAATTTGAACAGCTGCAGCTAGAAATGGCTTTCCCTGTGTATGAACCTGGCA
 AAGACAGTTTCTCATCAAAATTAAGAGAGAGCCAAAGGCACCTAGCAAACTGCAATGCC
 ATTTGGTGAATCTGTGACTGTGTCTGAAGGACATCAAGGAGACCAATTTGATGTCAGCTG
 AGATGAGCACCTATCTGGTGGCTTTCATCATTTTCAGATTTTGGATCTCTCAGCAAGATAAC
 AAGAGTGGAGTCAAGTTTCTGTATTGCTGTGCAGACAGAGATAAATCAAGCAGATATTC
 ACTGAGTGCTCGGGTGATCTCTAGAAATTTATGAGAGTTTCTCAGTATCATGATCTCC
 TACCAAAACAAGATCTTGTGCTGTTATCCCGAATTTTCAGTCTGTGTGCTATGAAATGGGA
 CTGACAACATATAGAAATCTGCTCTGTGTGTGTGATGCAGAAAGTTGCTCATGACATAA
 GCTTGGCATCAGTGCAGCTGTGCCCAAGACTGGCCCACTGAGTGTGTGGGACCTGTGTC
 CTATGGAATGGTGAATGATCTTTGGCTAAATGAAAGTTTCTGATTTATTTGAGGTTTGT
 TCTGTCAGTGTGCCCATTTGAAATGAAGAGTGGAGATATTTCTTTGGCAAACTTTTGA
 CGCAATGGAGGTAGATGCTCTTAAATTTGATGACATGAGTCTACCTGTGGAAATCTGT
 CTAGACTCGGGTGTGCTGCTATTTCTCTATGATAAGGAGCTGTATTTCTGTAATTTG
 TTAAGGGAGTTCTTAGCTTCCGCAATTTAAAGTGTGTTGACAGTATCTCAGATGATCA
 TAGCTATATATACAAAAAGAGGACCTGTGGGATAGTATGCGAAGTATTTGCCCTACAG
 TGGCTTGAAGAGGATGATGGCTTTTGTCTAGAAATCAACATCTATCTTATCTTCAT
 TCTCTACGAAGGGGTGGATGTGAAACCAATGATCAACATTTGACATCTCAGAGGGGTTT
 TCCCTAATTAACATACAGCTCAGGGGGAGGAATGTACACTGAAGCAAGACATCATGTA
 AGGCTCTCAGCGGCCCGGCACCTTGGGTACCTTGTGGCATGTTCATTTGACATTCATCC
 AGCAATCAACATGTCTCATGATTTTGTCAATAAACAACAGATGTGCTCATCTCCC
 AGAAGGTTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATTTGTCATTAG
 AGAGTATGGATGGGACTTTTTCATGGCTTTTAAAGGAACACACACAGCAGCTCAGCAGT
 ATGATCTGGGCAAGTCTATTAAACAATGCATTTCACTCGTCAGCATTTGGGAAGTGTGCAT
 TGAAGAGGCTTGATTTATCTGTACTTGTAAACATGAAAATGAATTTGCTGGCTGTTC
 AAGTTTGAATGAGCTGATTTCTATGTATAGTTTGAATGGAAGAAAGATATGAATGAAGT
 GAAATCAATTAAGGCTCTCTCATAGGCTGTAAGGACCTCATTTGATAGACAGCATAT
 GACAGCAGGAGGCTCAGTCTCAGAGCAAACTGCTCGGAGTGAACTACTACTCTCGCTCTG
 TGCACAACATCAGCGCTGCGTACAGAGGGCAGAGGCTATTTCAGAAAGTGAAGGAATCC
 AATGAAACTTTGAGCTGCCCTGTGCAGCTGACCTTTGGCAGTGTGTGCTGTGGGGGCCGAG
 CACAGAAGCTGGGATTTCTTTATAGTAATAATCAGTTTCTTTGTCAGTATGAGAAAT
 GCGAAATGAATTTGCCCTCTGCAGACCCCAAAATTAAGAAAGCTTCAATGGCTACTAGAT
 GAAAAGCTTTAAGGAGATAAAATAAAACCTCAGGAGTTTCCACAATTTCTTACACTATTGG
 CAGGAACCCAGATAGATACCACTCGGCTGGCAATTTCTGGAAATAATGCAACAAACTTGG
 TACAAAAGTTTGAAGTTGGCTCATTTCTTCATAGGCTTCAATGGTGAACACAAATCAA
 TTTCTACAGAAGAACCGGCTGAAGAGGTAAAGGATTTCTCAGCTCTTTGAAGAAATATGG
 TTTCTCAGTCCGTTGTGTCCAACAGACAATTAAGAACATTTGAAGAAACATCGTTGGATGG
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTCGAAAGTGAAGAGCTTGAACGCTATGAA
 TTTCTCCCTTTGCCGGTTCTGTGTTCTCTAATACCAACATTTTGTGTAGTGTATTTCAA
 CTAGAGATAGGCTGTGTTTGGCTCCAACCTGGAGATACATTTTCCCTTCAACTCATTTTGTGA
 CTATCCCTGTGAAAAGAAATAGCTGTAGTTTTCATGTAATGGCTTTTTCATGAATGGGCTA
 TCGCTACCATGTGTTTGTTCATCAGAGTGTGGCTCTCAAGCTAAACCCAAAGTGTGGGT
 TCCCTGCCACAGAGAATAATGATACCTTATCTCTCAAAAARAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTFPPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQVLE
 HPPQEQIALLAPEPLLVLGPLYTVVIHYAGNLSETFHGFIKSTYRTKEGELRILASTQFEPTA
 ARMAFFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMGDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRELLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMEKRDMEVETQFKAFLIRLLRDLIDKQWTWDEGVSVEQMLRSELLLLACVHNQPCV
 QRAEGYFRKWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSTEKSQIEFALC
 RTQNKELQLWLLDESFGDKIKTQEFFQILTLIGRNPVGYPLAWQFLRKNWNKLQKFELGS
 SSIAHVMVGTNTQFSTRTRLEEVKGFFSSLLKENGSQLRCVQQTETIETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteinases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**ATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCTAGTATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
 GCTGCAAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTCAAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG
 GGATCTTCTCTGCGCGGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGCCCTTCTGCT**TAA**CTCTATTACCCCCACGATTCTTCACCGCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACAAATCATTATCTACTCACCTAACAGCA
 ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCTCTTCA

FIGURE 250

MSAVLLALLGFIPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTCYDGLLRRLGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES LTWVGVLALAPALWWGVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCCTGCGCT
 CAGC**ATG**AGGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCGTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGCGCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCTAT
 GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTTCATCAAGAATGCTGTGCGC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCACAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGAGATGTTGGCCT
 CGGGCGGCTGGAACGAGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATC**TGA**CGCCTCAGGCTGGGGCTGCCCATTTGGGGGGCCCCACATGTCCTTGCAAGGGTT
 GGCAGGGACAGAGCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGGTGTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTGCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

MRGNLALVGLISLAFSLPSGHPQFAGDDACSVQILVPLGKDAGEKGDKGAPGRPRGRVG
PTGEGDMDGDKGQKGSVGRHGKIGPTGSKGEKDSGDTGPPGPNGEPLPCECSQLRKATGE
MDNQVSQLTSELKFKINAVAGRETESKIYLLVKEEKRYADAQLSCQGRGGTILSPMKDEAAN
GLMAAYLAQAGLARVFCEIDNLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNVDVACHTTMYDFMGFDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
 TTCCTGGCGGGGGCCGACGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCCTCGGCCC
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCGGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAACTGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTAGAGTTCTCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCCCTCAACAATAAAGGATTTTTCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEKGTGPFLLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCCGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGGTGGTGTGCATCCCCCTTGGGGC
 TGCTGTTCCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACCTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGC
 CTGGGCCACCGCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGGTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCATGCCCTG
 AACCT**TAG**ACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAAGTCTTAGGCTCAAGCAATCCTCCTGCCCTCAGCCTCTCAAAGT
 CTAGGATTATAGGCATGAGTCACCCCTGCTCTGGCTCTGGCTCTGTTCTTAAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCCTTACATGCTACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTCTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG
 CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGGCTCAAGGTCAACCCCTCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG
 GTCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
 TTTAAACAACCACGCTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCAGCTGCAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCAAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTILLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GGG
GTCTGGGCTGCCCTTGTCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGCCCGGGCTTTTGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCCCTCCTGAGTGGCAATAAATAAAATTTCGGTATGCTG

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FIGURE 258

MGSGLPVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT



FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCGTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCACTGTTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCTTGAAGCCAATGGAATACCTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAAATAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

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FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECIVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

GAGGATTTGCCACAGACGCGGATAGAGCAGGAGACACACCGGAGCCCTTGAGACATCCTT
CAGAGAGGACGACGATTAAGAGACATGCCCTGCTTGGTGTTTTGCGAGCATGATGCTGGCCGCTT
CGAGGAGCTTTGCGATTGCTGGTGTCTGTTCTTTCGAGCTTTTGTGCCCCGGCCGACGTATAC
CCGAGGACCGGACCGATGGTGCTATTCATCTTACCAGGCTTTTCGAGTTCTGGAGCAGAGGCTGG
AAAAATTGTACCAAGCACGAGGGCATACATCTCAAGAATTCAGAGTTCTCAAAAATAATA
TCTGTTCATGCTGGGAAGATGTGCAGACTACACAAGTGAGTACAAGGTGCAGTGGGTAACCTT
GGCAGCTGAGAGTTGAACGTGCCAACGGAGATTGACTACATACAATACCTTCGAGAGGCTG
ACGAGTGCACTCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
GTTAAAAAGATCGCGGACTGCTGCTGAATCGAAGCTGTGACAACTGCTGATGGGCATAAAGCT
TTTTGAAATAGTGAAGAAGATGATGGAACACATGGCTCTTGGATGAAGAATGCTGTCTATA
ACTCTCCAAAGGTGTACTATTATAATTGGATTCCAGAAACCAACTGTTTGGGAATTGTCAAAAC
ATACGGGCTTCACTGAGGATAACACAACGACACTCCCGGCAAGCAAACTCTCAACACTTTC
CTGGCAGGGAACAGGCCAAGTGTACTTACAAGGTTTTCTATTTTTTTCAATCAACCAAGCAACT
CTAATGAGATAATCAATATAAAGCTGCAGAGAAGGACTGTGGAAGTCAAGTCTGCTCCCA
GGAGGGGTAGGCGGAGCATTGGTTTACAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
GGATGAGCATGGGCTCTGGGCGCACTCCACTCTGGGCGCAAGCCCATAGCCATTTTGGTCTCA
CAAGAGTTGAGCGGGGCACACTGGGAGTGAGCACTCATGGGATACCCATTGCAAGAAGCCAG
GATGCTGAAGCCCTCATTTCTCTTGTGTGGGTTCTCTATGTGTGCTACAGATTCTGGGGCCCA
GGGCCCTCACTGCATCACTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGAGCACTTGC
CCAACCTGTTCTTCCCAAGAGACCAAGAAGTCACTCATGATCCATTACAACCCAGAGAT
AAGCAGCTCTATGCCCTGGAATGAAGGAAACCCAGATCACTTACAACCTCAGACAAGAGAA
GCTGCTCTGAACTAAAGTCAATTACAGCTGTGAGAAGAGCACTGTGGCTTTGGCAGCTGTTC
TACAGGACAGGTGAGGCTATAGCCCTTACAATATAGTATCCCTCTAATCCACACAGGAAG
AGTGCTGAGAAGTGGAAATACGATGCTCCCTTTCCCAAAATGTCACTGCTTATGATATCTTC
CAAGAGCTTAGATGAGGACGATATCATCAGGAAAGTTTCAACATGTCCATTCTCCCCAAA
CCTCTGGCTCTCAAGGATGACCACATTCTGATACAGGCTCACTTCAAGCCTTTTGTGTTTACT
GCTCCCCAGCATTTACTGTAACTCTGCCATCTTCCCTCCCAAAATAGAGTTGTATGCGAGC
CCCTAAATATTCACCACCTGGCTTTCTCTCCCTCGCCCTTTGCTGAAGCTCTTCCCTCTTTT
CAATGTCTATTGATATCTCCCAATTTCTACTGCCAACTAAAACTATTAAATTTCTTT
CTTTCTTTTCTTTTCTTTTGAGACAAGGCTCACTATGTTGCCAGCGCTGGTCTCAAACTCC
AGAGCTCAAGAGATCTCTCGTGCTCAGCCCTCTTAAGTACTGGGATTACAGCATGTGCCAC
CACACTGCTCTAAAACTACTATTTCTATTGAGTTTAACTCTATTTCCTCAGGCCCTGTC
TCTTCACTAAGCTTGGTAGATGTAATATAAAGTGAATAATTAACATTTGAATATGCTTTT
CCAGGCTGTGAGGTGTTTGACATCAITGAAITCTGTTTCACTTTGTGGAACATGCACAG
TCTTTACAGCTGTCACTTGAGAGTTAGTGAGTAACACAATACAAGTGAAGAATACAGC
TAGAAAACTACAAATCCCATAGTTTTCCATTGCCCAAGGAAGCATCAAAATACGTATGTT
TGTTCACTTACTCTTATGATGCAATGGCTCATGTTTTCAGCTCAAAAATAATGATCTGTCCC
TTTAGCCAGTTTTCATGTCTGCACAGACCTTTCAATGAGCCCTTTCAATGATAAATCTCC
AGAAAACCGGTCTAAGGCTGAGGACCCCAAGTCAAGCTCTGCTCTGTCTGTCTGTCTCTGT
TTCTCTTTCTCTGCTTTAAATTCAAATAAGTGACACTGACCTGACCAAAAAA

FIGURE 262

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKKKIIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTLQGTGQVIYKGFLLFFHNQATSNEIKYNLQKRTVED
RMLLPGGVGRALVYQHSPTYIDLAVIDEHLWAIHSGPGTHSHLVLTKEPGLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGPFRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

FIGURE 263

GGGCGCCCCGTACTCTAGCTGAGGTGGCAGTGGTTCACCAAC**ATG**GAGCTCTCGCAGA
 TGTCGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGG
 GTAGCGGGGGGTGGCTGCGCGGGGGGAGGAGGAGCGGCCGGCCCCCTGCCAAAAAGC
 AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATT
 GGAAGGAGAAGCCTCAACAACAACCTTCAACCACCGCCTCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCAAGGACTTCCTGCAGCGAGAGCACCGCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTACAGCCACCCAGAGGACTTCCTAAAAAGCACAAGGCGCCTGTCA
 TCGACATTGGCATTGTCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACAGATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTTCACCCCAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGAGCCTTCGAA
 CTAAGGGGCCACTCCGCGGCTGTGCCTCGTTTGTCTTCTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGTTACATGGAACCTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGTCTGAAGACAGGCCGCTTTGAAGAGGCGGGGGTGCCTGCGCGCTGCCG
 CTGGCCCTCTCCCCAACCGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCACTCTTA
 CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGGCTG
 TTTCAACAACCTCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCCTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TGAC**CTCTGGGAGGGCCCGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCTCCCAAGGTGGAAGCCTTTCAGAAG
 AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCCATTTGAACCTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTCTGGCTGTGACTCTCCCTGACTAGTGCCCAAGGTGCTTTTCTTC
 CTCCCAGGCCAGTGGGTGGAATCTGTCCCACTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCTTGTGGCAGCACATCTCACACCCAAGAAG
 TTTGTAATGTTCCAGAACAACCTAGAGAACCTGAGTACTAAGCAGCAGTTTTGCAAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAAGTGTGTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCTCAGTTCTATTGTGAAGATGGAGAATAATCTCTCTGTGAACCTCCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT
 AGTACTATTGTCCAATGTCATGAAAGTGGTAAAGTGGGAACCACTGTGCTTTGAAACCAAA
 TTAGAACAACATTCCTTGGGAAGGCCAAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTCGGGAGATGATATCTGTGTTTAAAGGAGACCTTTTTCAGTTTCATCAAG
 TTCATCAGATTTTGAAGTGCCACTCTGTGCCCAAATAAATATGAGCTGGGATTAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFI VWLANGDTLRVFKMTKREDGGYTF TATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTT**TAG**CGCTTGCTGCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCCTCCCCAGGTGACCTGCTCTCTTCTGGGCCCTG
 CCCCTCTCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCTCAGGCCCTTACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGGCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTGATGCCTCTGAGGCCCTCTTACCACACTTTACAGT
 TAACCACTGAAGCCCCCAATTCACACAGCTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTTCCTTAACAACCTCCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52



FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAGGCCGGCAGAGGGAGGCACTTGAGAAATGTCTTTCTCCAGGACCCAAGTTTCTTACCATTGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGCGTGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTCTGTCCAAGCCCCAGAAAGCCGCCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAAGCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTGTGCGAGAGGAAGCTGCGGATCTGTCTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGATGATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCAGGAAAGCAGGGCATTTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACTTTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAGAAAAATGATTGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTATGGGATGATTTGTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTAATAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGACAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAAATTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAGGTGCGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTACTATAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCAGCTACCCGGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGCTGAGCTGAGATCACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTFLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCCTTCATCCACCAGCTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGCTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLGLLLALGLPFLLARWGRAWGQIQTTTSANENSTVLPSTSSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLEKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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FIGURE 271

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAAATGACATTTTTCTGTCACTATTATTATGTG
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSGCLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPTPPPPVFSLLKISQRIVCLV
 LDKSGSMGGKDRNLNRMNQAAKHFLLOTVENGSWVGVMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGDNNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMKNKDVNSFSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGRYSLKVRAGH
 GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDTSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTVHEDKIILTWTA PGDNFDVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCTGGGAGTAGAGTACTGACAGCAAAGACGGGAAAGACCATACGTCGCCG
GGCAGGGGTGACAAACAGGTGTCACTCTTTTGTATCTCGTGTGTGGCTGCCTTCTTATTTCAAGGAAAG
ACGCCAAGGTATATTTACCCAGGAGGAGCAATGATGTAGCCACCTCTTAACCTTCCCTTCTTTGAACC
CCCACTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT
GTGGTTGGAGGAGAGAACCTTTGTGGGGCTCGGTTCTCTTAGCAGTGTCTCAGAAGTGACTTGGCTGA
GGGTGAGGAGAGAAAGGAAAGGTCCCCCTCTTGTCTGTTGGCTGTCACCTCAGGAAGGCTGTGATGGG
AATGAAGCTGAAAACCTTGGAGATTTCACTTCACTGCTCATTGCTCTGCCTGCAAGATCATCTCTTAAAA
GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGT
CAAGCAGCTCCGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGGG
GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTCTGAATGATGATGGTTCGCC
GGGGGCTGCTTTCGTGGATTTCCCGGGTGGTGGTTTTGCTGGTGCCTCTGCTGTGCTATCTCTGT
CCTGTACATGTTGGCCTGCACCCCAAAGGTGACAGGAGCAGCTGGCCTGCCACGGGCCCCAACGC
CCCCCGGGGAAGGAGGGGTACCCAGGCGCTCTTCAGGAGTGGGAGGAGCAGCACCCCACTACGCTGA
CGAGCCTGAAGCGGGCAGATCCGACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTCAAGCAGCTCAGGA
TGGGCGAGTCAACGAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCGCCAGAAACCCAG
GCCACCTCTCTGGCTTCTCTGCACTCGCAGTGGAGTGGACAGGACAGTGAATGCTGGCTCAAGCTGG
CCACAGAGATGTCAGCAGTGCCTTTCCGATAGCTTTACTCTACAGAGAGGTGACCACTGGAGACTGG
CCTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGAGTGAAGTGGTGAAGCCATT
GAATCAGCCTTGGAGACCTTGAACCAATCCTGCAGAGAACAGCCCCAATCACCGTCTCTTACAGGCCCT
CTGATTTCTATAGAAGGGATCTACCGAACAGAAAGGGACAAGGAGTATGTTAGAGCTCACTTCAA
AGGGGACCACAAACCAAGTTCAAACGGCTCATCTTATTTGCACCATTCAGCCCCATCTAGAAAGTG
AAAAATGAAAGGCTCACATCTGGCCAAACAGCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGG
ACAAAGTCCCGCAGTTCATGCAAGAATTCAGGAGAGTGTGCATTTGAGCAGGATTTGGAGAGAGTCCATCT
CACTGTTGTTTACTTTTGGGAAGAAGAATAAATGAAGTCAAGGAATAGTTGAAAACACTTCCAAA
GCTGCCAAGCTTCAGGAAGCTTTTACCTTCACTCCAGCTGAATGGAGAATTTCTCGGGGAAGGAGACTTG
ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGCTCTCTCTTTTCTGTGAGTGGACATCTACTT
CACATCTGAATTTCTCAATACGCTTAGGCTGAATACACAGCCAGGAGAGAAGGTATTTTATCCAGCT
CTTTTCAGCTCAGTACATCTCGCATATATACGCCACCATGATGCAGTCTCTCCCTTGGACATCG
AGCTGCTCATAAAGAGGAACACTGGGTTTTGGACAGACTTTTGATTTGGGATGACGTTGCAGTATG
GTACAGCTTCATCAATATAGTGGTGGTTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGTCAC
CTTTATCGCAAGTCTCTCCACAGCAACCTCATAGTGGTACGGACGCTTGGCAGGACTTCTCCACC
TCTGGCATGAGAAGCGCTGCATGGACAGCTGACCCCCGAGCAGTACAAGATGTGCATGAGGCTCAA
GGCCATGAACAGGAGCATCCCACGGCAGCTGGGCATGCTGGTGTTCAGGCAAGATAGAGGCTCAG
CTTCCGCAACAGAAACAGAGACAAGTAGCAAAAAACATGAACTCCACAGAGAAGGATTTGGGGAGA
CACTTTTTCTTCTCTTTTGCRAATTACTGAAAGTGGCTGCCAACAGAGAAAAGACTTCCATAAAGGACG
ACAAAAGAAATGGAGCTGATGGGTACAGATGAGAAAGCTCCGATTTCTCTTGTGGGGCTTTTTAC
AACAGAAATCAAAATCTCCGCTTTTGCCTGCAAAAGTAAACCAAGTGGCCACTGTGAAGTGTCTGACA
AAGGCAGAAATGCTGTGAGATTTAAAGCCTAATGGTGTGGAGGTTTTGATGGTGCTTTTACAATACAT
GAGACCTGTGTTTTGTGTGCTCATTTGAAATATTCAATGATTTTAAAGCACTTTTGTAAAAATTCAT
TAGCATGAAAGGACAGCATATTTCTCTCATAGTGAAGGAGATAGGCTTATTATGACTACTAGTAGTACATTAAGTA
AAATAAAATTTGGACCAAGAAAGAAAGCAAAACCATAAATCTCGTGCATATTTTCCCAAGATTAACCA
AAAAATATCTGCTTATCTTTTGGTGTCTCTTTAACTGTCTCGGTTTTTTTTCTTTTATTTAAAAAT
GCACITTTTTTCCCTTTGTGAGTTATAGTCTGCTTATTTAATACCATTCTGCAAGCTTACAAGAGA
GCACAAGTTGGCCTACATTTTATATTTTTTAAGAAGATACTTTGAGATGCATTTATGAGAGCTTTCA
GTTCAAGCATCAAAATGATGCCATATCCAAGGACATGCCAAATGCTGATTTCTGTCAAGCACTGAAT
GTCAGGCATTTGAGACATAGGGAAGGAATGGTTTTGACTAATACAGACGTACAGATACATTTCTCTGAA
GAGTATTTTCGAAAGGAGCACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA
AAGGAAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAGTCAAGAACCCACATTTTCTCCTCA
GAAATAGGAGACCGCTTTCTTACCTGTTTTAAATAAACCAAAGTATACGGTGAACCAACACATCTCT
TTTCAAAAGAGGGTGCTCCTCTGGCTTCTGGCTTCCATAGAGCAAAATGCAAGAAATATATATAT
ATATATATATATTTGGAAGATCAATCTTCCAGCAATCTAGTGGATGGAAATATATATATATATAT
ATATATATATATTTGAAATTTGCAATCTGAACTGAATTTTAAAAATTAAGCAGTTCTACTCAATCA
CCAGATGCTCTGAAATTTGCATTTTATACCATTTCAAACATTTTTTAAAAATTAATACAGTTA
ACATAGAGTGGTTTTCTTCACTGTGAAATTTATAGCCAGCCAGATGACATGAGCTAAATTTCT
CTTTGAGTCCTTGTCTGTTTTGCTCAGTAACCTACTGTTTTAAAGCTTCAAGAACATCAAGC
TGTTGGTGTGTTAAAAAATGCATTTGATTTGATTTGACTGGTATGTTTGAATTTAATTAACAC
AGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

FIGURE 276

MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPFI
MKVKNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSQYNPGIYYGHDAVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVVRLFHLWHEKRCMDELTPQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT



FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTATGATGCCTTCATGAAGAGGATGAGAGGCTACCCCCTCTCTGAAGGGCTGT
 TGTTCCTGCTTCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTCCTCTTTTGTAAATAAATTTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAAGCTATTACAGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCCTAATAGGAC
 AATTCTAATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
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FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGCTGTCACACTGTA
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACCTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA
 GTGTAAATTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTGGCCTTAA
 GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTACATTTTCCTTTACAGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTTCCCTTCCACATTCTCAATTTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATCAAAGTAAATGACATTTTATTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCAGGTGATAGATT
 TTTGTGCG

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQVFVYHYIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPDPDVGIVIGIRLSVVHTVRFSEIHFLALALGSAALMIIVIVVVLQHYRKKRWAER
AHKVVEIKSKEERLNLQEKVSVYLEDD

FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGCTCCCT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTC
ATCCAACACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAA

FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCCTCCTTGCCGAGAGA
GTGTCCTGGGTGAGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAACACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAACTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 285

GT**CATG**CCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCAGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGACAAATAGAACTCTGGGGCAGGAGGTGAGC
CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCCTCCACGCC**TGA**ATCTGCCTGGATGGAAC TGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CTGTTTACTGGGATCAGCCAGGGCGCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
CAGGCGGGGACAAAGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTTCATGCCTACACACCCTCATTAAGCAGAGTCTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELGQEVSRGRDAAQELRASLEETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ
IQERLHTAALPA

GGCAACATGGCTCAGGCGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
CCTGGTGATCACCTTACTCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
AGCACAGCAAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
TGGACAGAAGTCAATGCCTTGAAGGAAATTAAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
AAGACTGCATTTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
CTCCAAGACTATGGTAAAAGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
CATGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGG
ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACTGTGTCTCTTCTCCCAATCAGCTCAG
GGCAAGTGGAGTGATGAGGCCCTGTCGCAGCAGCAAGAGATACATATGCGAGTTACCATCCC
TAAATAGGCTCTTCTCCAATGTGTCTCCAAGCAAGATTATCATAACTTATAGGTTTCATGA
TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATTTGCAACACAAGATCAAT
GTCCATAGCAATATGATAGCATCAGCCAAATTTGCTCTAACACATTTCTTTGGGATTTTGCCCT
TCTCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCGACATAAAATGGCTTCTGCT
AAACAGACATAAAATCTTTCTCTCTAGTCTTTCTCACTGTACAAACCCAGTTTGTTTTCAA
AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
GCTATATAATCCAAAAACTTTTCAGCCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
TTGTGAGCCCATACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCT
GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCC
TACCTTTTTTTTGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGATATTTGAT
CAATTTTCATTCCCACCATTGCAATTACAACCTCTAACCTTAAATGGGTAAACCTAAGGCATAT
CAAAGAGCGAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTT
TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTT
TGGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGAAAATTGCATACGCTGTGCAATT
TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAACTCATGCT
TAATATCAAATTACAAGTTTAGACTTGGAGGGAATGGGCTTTTAGAAGCAACAACATTTT
AAATATTTTGTCTTCAAATAAATAGTGTTTAAACATGTAATGTGTTTGTGAAACAATAT
CCCATTTTGCAACCTTAACTACACATGCTTGGAAATTAAGTTTGTAGTGTTTTCTTGTCTCA
ATAATAAGCCTGAATTTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCCGCAGGTTCCCCGCGCGC
 CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCCTGCA
 GCTCCGCTGCTGCTTTCCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCGCTG
 GAGTCGGCGGCGAGGCCGGGGCCGGGACCTTGGCCAACCCCTCGGCACCCCTCAACCCGCT
 GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT
 GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
 GCCCTGACAGTGTTTGGCTTCAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
 CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCT
 CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

TG AAGGAC TTTTCCAGACCCCAAGGCCACACCTGGAAGTCTTGCAGCTGAGGGGAGGCATC
CTCTTGCGCTCCGGCAGCCGATCAGCAATGAAGGTGGTCCCAAGTCTCTGCTCTCCGCTCCCTG
GCATAGGCTGGGTGGTGTACCGCGCTTGGCCCGGCTCCTCAGTCGCAGACAGACCCAGCCCC
TCAGAACACAGACAGCAGGGTATGTCAGGCTCCAGGAGGAAGAGGAAGATGAGCAGGAGG
CCAGCGAGGAGAAGCCGGTGAGGAAGAGAAAGCTGGCTGATGGCCAGCAGGACAGGCT
GCCAAGGACACTTCAAACCTCGGAATCAGCCTGCTGCGAAGAACTCCATGAGGCACGATG
CAACATGGTCTTCTCCATTTGGCATGTCTTGGCCATGCAGAGGCTTGATGCTGGGGGCA
CAGGCGCGCATGAACCACAGATCAAGAGAGGGCTCCACTTGACGGCCTGAAGCCCAAGAA
CCCGGGCTCTGCTCTCTTTAAAGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
GGGCTCTCAGCAGGGGAGTTTGCCTTCTCCCAAGAGTTTGGTGTCAAAGAGACTTCT
TCAATTTTCAAAGAGTATTTGATACAGAGTGCGTGCGTATGAATTTGCGAATGCCCTA
CAGGCCAAAGAGGCTCATGAATCATTACATTAACAAGAGAGCTCGGGGGAAAATTTCCAACT
TTTGATAGAGATTAATCTGAAACCAAAATTAATTTGTTGGATACATCTTGTTCAAAGGA
AATGGTTGACCCCAATTGACCTGTCTTACCCGAAGTCGACACTTCCACCTGGACAAGTAC
AAGACATAATAAGTGGCCATGATGTACGGTGACGGAAGTTGCTCCACCTTTGACAGAA
TTTTCGTTGTCTGTCCTCAAACCTCCCACTACCAAGGAATGCCACCATGCTGGTGCTCTCA
TGGAGAAAATGGGTGACCACCTCCGCCCTGAAGCATCTCTGACCACAGACTTGGTGGAGACA
TGGCTCAGAAACATGAAACCAGCAACCTGGAAGTTTCTTCCGAAGTCAAGTCATGATCA
GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAACTTCTCACCTTTG
CTGACCTTAGTGAACTCTCAGCATCTGGAAGAAATCTCCAAGTATCAGGTTTTCAGAAGA
ACAGTGATTGAAGTGTGAAGAAGGGCAGTGGAGCGATGGCAGGAATCTTGTCAAGAAATTAC
TGCTTATTTCCATGCTCTCTGTATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
AAACCTCTGGAATGCTTCTGTTTCTGGGCGAGGTGGTGAATCCGACCTCTCTATTAATGAG
ACATGCATAGACCACTCTGCTGTGATAGTATGCTGAATCGAGGTATCAACACACACAGGA
TACAGCAATGGATGGCAGGGGAGAGTGTCTTTGTTCTTAACTAGTTTATAGGTTGTTCTC
AAATAAATACAGTAGTCCCCACTTACTTGAGGGGATACATTCAAAGACCCCGACAGATGC
CTGAACCGGTGGACAGTGTCTGAACCTTATATATATTTTTTCTCATACATACATACCTATGAT
AAAGTTTAATTTATAAATAGGCACAGTAAGAGATTAACAATTAATACAACATTAAGTAAAA
TGAGTTACTTGAACGAGCACTGCAATACCAATACAGCTCAAACTGATTTAGAGAAAGGCTA
CTAAGTGACTCATTTGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGGCAAGGGGAGATTC
CATCTGGTGGGACAGAGCAGGACGATGCAAGATTCCTACCTACTCAGATGCAATGCA
TGCTTAAGACTTTTGAATGTTTATTTCTGGAATTTTCATTTAATGTTTTTGACCATGGT
TGACCATGTTTACTAGTGCATGCAAGAAGCAAAACCTGGATAGGAGGAGCTACTACAAA
GCATTAATTTGATACATATTTTAAAAAAAAAAAAAAAAAAAAA

MKVVP S L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
 E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
 K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
 D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
 V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V L M E K M G D H L
 A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
 T G R N L Q V S R V L R R T V I E V D R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H M I Y E E T S G M L L F
 L G R V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGAC**ATG**AG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGCTGTTCCC
TGTCAGAAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCTGGGCCGTGTCCTGAGTCCC
GAGCCCAGCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGAGGAAGACCAAGACCACA
TCTACCACCCCA**G**TAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAGGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

MRRLLLVTSLVVLLWEAGAVPAKPVIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRQGGRGILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGE
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAAATGAACCAACTCAGCTTCTCTGC
TGTTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCAATGAGAATGACATG
CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCCAGAAAACAGCATCTTATTACTCACCCATGGCCAGCGGGAATCACTGCGGGGATT
TGTTTCAGTTTACGGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACATCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAAACCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGFVIPVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL
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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACA**ATG**GGACTCGGCGCGCAGGCTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGAAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAAACAACAGTGTTTACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATT**TAA**GGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGATTACGTAATATGT
 AAGATTCTTCAAGGTAACAAGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAATACTCC

FIGURE 298

MGLGARGAWAALLLGTQLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCG**GATG**GCGACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCCGTGGCGCTTTCGTGCTGCTGCTGGC
 GCAGCTGTGAGAGCCGCCAAGAATTTCGAGGATGTGAGATGTAATGTATCTGCCCCCTCCCT
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCGTGCGGGGGCCTGATGTAGAAGCACTACTGTCTACGCTGTGA
 ATGCAAAATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAATATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTTTGACCGG
 CATGTTGTCTCAGCT**TAA**TGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAAGTACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTCACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAACCTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCTATTG
 TGACTTTTACTAATAAAAAATAATCTGCCTGTAATATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTG
 TTGTTGTTGTTTTTTGTTGTTGTTTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT
 AACAACTTTTTTCAAGTCACTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACTGACTGTATTTATCTGGGTATCTGCTGTGCTGCACCTCATGGTAAACGGAT
 CTAATAATGCCTGGTGGCTTTTACAAAAAGCAGATTTTCTTATGTACTGTGATGTCTGATG
 CAATGCATCTTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATATTTGGATAACTGGCTTTTT
 TCTTCCTATGTCCTCTTTGGAATGTAAATAAAAAATAATTTTGAACATCAA

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYKNIS QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII
IYLSILGLLLLYMVYLTLEVPI LKRR LFGHAQLIQSDDDIGDHQPFANA
HDV LARS SRANVLNKVEYAQQRWKLQVQEQ RKS VFDRHVLS

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FIGURE 301

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCAAGGCCTTCCTGTCCC GCGGGAAGCGG
CAGGAGCCGCCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA
TCATTGTCTACATTA AAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTAGTTTCACATAAGAATG
TTTACTCAATGTTTAAAGTGT TTTGCCCCAAAATTCACAAC TAACAGGCAGAACTAGGACTT
GAACATGGATCTTTTGGTTCCTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRPPMMHHHQAPSDGQT
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFGIFLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGAGATTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCCTTGGGCCTGAATTGACTTGAATGTTTCCCCGCTGAGCTAACAGTCCATGTG
 GGTGATTCAAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTTCAAGAT
 AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACC CGGTACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAAGTGGGATGTGTTTTCCAG
 AGCACAGAAGTGAAACAGCTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTCTGTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTTCCATCATG
 CTTCAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACTT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAA
 GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTTGAGAAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCTCCTGTGTGTGTCCTGGGCCACTCTACAGTGATTTCAGACTCCCGCTCTC
 CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
 GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYSNLSVPTIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKL RMSVEYSQSWG HFQNRVN LVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLPLVLILIVKKTCGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSP IIVREVIEEEEEPSEKSEATYMTMHPVWPSLR
SDRNN SLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATGTAAGAGTTGG
AAACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA
GGATGAAGATGGATACATCACCTTAAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTGGTCTGTCATGCAGCGCAATTACCTACAAGA
TGAGAATGAAAATCGCACAGGAACCTTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
TAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGACACAAAC
TGGAGATATTATGGAGATAGCTGCTATGGGTTCCTCAGGCACAACCTAACATGGGAAGAGAG
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG
AGAACAACACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPAIVSVGPASSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

CCACACGCTCCGCGCAGTCTCGCGAGTTCTTGCCTCCGCCTGCCAGTCTCGCCCGGATCCCGG
CCC GGGGTGTGGCGTGCAC TCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCAG
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
GCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCTCGCAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGACAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGCGCGCGGTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTCTCAGCAGCCCCAGCAAAGGCCAAGACCAGCTGC
GACAAAACAAGATTAAATCTTTTCCGGTGCCTTCAACTCTTCGGCTCCAAGAAGAGCGCAG
AAGAAGACAGAGCGCTCAGCTTAAGGTATAGTTAACCAAGTATACAGCCGACAGGCTACC
ACTTGACGCTGCAGCGGATGGAACCATTGATGCGACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTACACCTGAGTGCA
AATTCAAAGAATCAGTGTTTGAATAATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAACCGCTGCAGCTCATTTTCTGCCTAAACCACTGAAGAGTGCCCATGT
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGCTCTGGCGTGTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAGGCTCTGTAACAGAGTCTTACCTCCAGGTCTGTTGAAT
TCTTCTAGCAGCTCTTCAACCAAAGTCTCAAAATTTGCTCAGTGACATTTACCAACAACAGG
CAGGTTCTCAATTTCTATCTGCCATAGACCTTCTTATCATCCATACATAAGC

FIGURE 308

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLRQKRQAREREKSNACKCVSSPSKGKTSCKNKNLVFSRVKLFSGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSSELFTECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSVSGVLNGGKSMHNEST

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTG
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC
 AAGAGTGGATTGGCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTAGGACAGACACTG
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCG
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGCCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAACCTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT
 GTGGGCCTCCGTGTGGTACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCCACTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLILLISKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLGANPDGSIQGTPEDTSSFTFNLIPIVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYVYLYASALYRQRSSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYOEPSLSVPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGGGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAAACAGA
GTAAAGAAAACCAAACAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAACCAGTCAACAAGAGTAAGACAACAT**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRLR
RQDPQLKGIVTRLYCRQGYLQMHPDGDGALDGTKDDSTNSTLFLNLPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAT
 GAAGGATGCAAGGACCGAGCTTTCTCTCGAACCAGCAACCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AAATAAACCGAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGAGGATTCAAAAGAAAAAGTATGTTTCATT
 TTCTCTATAAAGGAGAAAGTGAGCCAAAGGAGATATTTTGAATGAAAAGTTGGGGCTTTTTTAGTAAAGTAA
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAAAGAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCA
 CAGTTGGATTGTGCTATGTTGACTAAAATGACGGATAATTCAGTTGGATTTCCTTCATCAACCTCCTTT
 TTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACTGGATTTCATCT
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTGAATTCAGAAGGACCAACACAGATAAAATTAATG**ATG**
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCT
 GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCCCTCTCTGT
 GCTCTGCAACAACAGCTTACGCAAGGTGATTGTGTTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTC
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCATCTGAG
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGCTGCGCA
 ACCTCAACACTCTGGAACCTTTGACAACTGCTCTTACTACCATCCCGAATGGAGCTTTTGTATACCTGTCTAAA
 CTGAAGAGAGCTCTGGTGGCAAAACACCCCATGAAAGCATCCCTCTTATGCTTTTAAACAGAAATTCCTTCTTT
 GCGCCGACTAGACTTAGGGGAATGAAAAGACTTTCAATCATCTCAGAAGGTGCCCTTTGAAGGTCTGTCCAACT
 TGAGGATTTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGTATGCACCTTCAAAAAT
 GTGGATGATACAGTCCCAGATTCAAGTATTGAACGGAATGCCTTTGACAACTTCAGTCACTAGTGGAGATCA
 ACCTGGCACAAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
 TTACATCACAAACCTTGAACCTGTAAGTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC
 GAACACAGCTTGTGTGCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGTGACATTGGAGAGCTCGACCAGA
 ATTACTTACATGCTATGCTCCGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTGCGGCTCCACATCCTGACATCTGTATCTTGGATTACTCCAATGGAACAGTATGACACA
 TGGGCGGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTCAAAATGTAAGTGTGCAAGATA
 CAGGATGTACACATGTATGGTGAATAATCATCATTTGGTGTTTTGTGGCATCACACCACTGGCTGAGTGTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTCGACAGAGAAACCTTCACCATCCCACTGACTGATATAAACAGTGGGATCCAGGAAT
 GATGAGGTATGAAGACTACCAAAATCATCATTTGGTGTTTTGTGGCATCACACCACTGGCTGAGTGTACTGCT
 GGTCATTTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAGCCACCTGCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACACACAACAACAGTTAAACCAATAAATTAATACA
 CAGTTTCAGTGCATGAACCGTTATTGATCCGAATGAACCTTAAAGACAAATGTACAAGAGACTCAAACT**TA**AAACA
 TTTACAGAGTTACAAAACAAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAACAACAAAGAAATTTATTATTAAAAATTCATTG
 TGATCTAAAGCAGACAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI¹STNTRLNLHENQIQI²IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSK³LKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
YISEGAFEGLSNLYLNLMCNLREIPNLTPLIKLD⁴ELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNFWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRATSLTSVSWITP⁵NGTVMTGAYKVRIAVLSDGTNFTNVTVDQTMGYTCMVNSVGN
TTASATLNVTAATTT⁶PFYSYFSTVTVETMEPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTF⁷FTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDDEITGDT⁸PMESHLPM⁹PAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

CGCCCGGGAGCCCATCTGCCCCAGGGGCAAGGGGCGCGGGGCGGGCTCCCCGCCGACAT
GGGTGCAGGCACCTTCGCCGCGACCCCGAGCGCGCGCCGCGAGCTCGCCCGAGGTCCGTCCGA
GGCGCCGGCCGCCCGCCGAGCAACGAGCACTGACGGCGGAAGCGCCCGCTCGGGGATC
GGGA**ATG**TCCTCTCCTCTCTCTCTTGTCTAGTTTCTCTATATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGGAGAAAGGTCATTTTGCCCTGCCACCTCAACTCGGGG
TTCAGAAAAAGACACTCTGGATATTGAATTGGTGTCTCACCAGATAATTGAAGGAAACCAAAA
GTGGTGATGACTTACTTCCAGTCGTCTATGTCATACATAACTTGACTGAGGAACAGAAAGGCG
AGTGGCCTTTGCTTCCAATTTCTGCGAGGAGATGCTCTTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCACTCTTAAAAGTCTTATGAGGACATCAAGGCCAAGTGTGAGTTTGAAGGAGAGCTGAC
AGCAAGGAAGTGAAGCTGACTTTGCAAGTGTGAGTCATCTCTGGCAGACAGCCATTGTGTATT
ACTGGCAGCGGAATCCGAGAGAAAGAGGAGGATGAACGTCCTCTCCCAATCTAGGATT
GACTACAACCACTCTGGACGAGTCTGTGCGAGAATCTACCATGTCTCACTCTGGACTGTA
CCAGTGCAAGCAGGCAACGAGCTGGGAAGGAAAGCTGTGGTGGCAGTGAACCTGTACAGT
ATGTACAAGCACTCGGACATGTTTGCAGGAGCAGTGACAGGCTATGTGGCTGGAGCCCTGCTG
ATTTCCTCTTGGTGTGCTGCTACTTCCGAAGGAAAGCAAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTCTGTGAAACCCAGCT
CCTCTTCTCCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCCACCTCGCTCTCACAGAAAT
AGTGCTCAAGCCAGCCCGGGACATGTCTCAACTGACGACAGCAACCCAGCGAGGCTGGCCAC
CCAGGCATACAGGCTGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
CTAATCTGACCAACCTAGAAACCAAGGATGATCTCCCAAGCCAGAGCAGAGCTCTCCAA
ACGGTCT**TGA**ATTACAAATGGAATGTGACTCCACGCTTCTTAGAGTCAGGGTCTTTGGACTC
TTCTCGTCAATTGGAGCTCAAGTCACAGGCCACAACAAGATGAGAGTCACTCTAAGTAGCA
GTGAGCTATTGACGGAACAGATTTCAGTAGCAATTTCTTCTTACATACCAACAGACAAA
AGGATGTAAAGCTGATTCATCTGTAAAAGGCATCTTATTGTGCCTTTAGACCAGATGAAGG
AAAGCAGGAGTCCAAATCTAATTTGTGACAGGACCTGTGGTGGAAGGTTTGGGAAAGAGGTG
AGGTGAATATACATAAACTTTTAATGTGGGATATTTGTATCATGCTCTTTGATTACAAAT
TTCAGAGGAAGATTTGGGATGCTGTTGTAAATTTCTATGCAATTTCTGCAAACTATTGGATT
ATTAGTATTACAGAGTCACAGCAACCAACCAAGCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAAACATGTGCTCTTCTATTCTGACTTAAC
TCTATTGTGTCATAAGTTTGGGATATTAATTTCAAGGGGAGTTTGAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACCTAATCTCATTATTTGATATGAGCCCAAAATTAAC
TATGAAGAGGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAATATATAATTGGAGCAATTTGGATTTCCTCCCTCAAA
CAGATGCCTTAAAGGACTTCTCGCTAGATATTCTCTGGAAGGAGAAATACAACTGTCAATT
TATCAACGTCCTTAGAAGAAATCTTCTAGAGAAAAGGGGATCTAGGAATGCTGAAAGATA
CCCAACATACCAATTATAGTCTCTCTTCTTCTGAGAAAATGTGAACCAAGAAATTCGAAGACTGG
GTGGACTAGAAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGTGTGAGGTTGCAGTGGCCGAGATTATGCC
ATTGCATCTCAGCGCTGGGTGACAGAGCGGACATCCGTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLVSYYVGTGLGTHTEIKRVAAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKKDEREEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSIVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 317

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCTACCTGCAGCCGCCGCCACGGCAGCGCAGCCCA
 CCT**ATG**GGCGCTCCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTCGCCAGAAAGTTTGGATATCACTACT
 CCTGAAAGAGATGATTGAAACAGCCAAAGGGGAAACTGCCATCTGCCATGCAAAATTTACGCTTAGTCCCGAAGA
 CCAGCGGACCGCTGGACATCGAGTGGCTGATATCACAGCTGATAATCAGAGCTGGATCAAGTGATTATTTTAT
 ATCTCGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACAGGTATGATCTC
 AAATCTGGGTGATGCATCAATAAATGTAAACGAATTTACAACTGTGCAGATATTGGCCACATATCAGTGCAAAGTGAA
 AAAAGCTCCTGGTGTGGCAAAATGAAGATTCATCTGGTAGTCTTGTGTTAAAGCCTTCAGGTGCGAGATGTTACG
 TTGATGGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAGAGAGGTTCACTTCATTTACAG
 TATGAGTGGCAAAAATTTGCTGACTCACGAAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT
 ATCTGTAAAAAATGCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC
 AGTGCCTGTTGCGTCTAAACGTTGTCCCTCCTTCAAAATAAGCTGGACTAATTCAGGAGCCATATATAGGAAGT
 TTGCTTGTCTAGCGCTCATTGGCTTTATCATCTTTGCTGTGCTGTAAGGCGCAGAGAAAGAAAATATGAAA
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACTCCAAAGAGCCGTACGTCCTGCCAGAGCTACATCG
 GCAGTAATCATTCAATCCCTGGGGTCCATGTCTCCTTCCAACTGGAAGGATATTCGAAGCTCAGTATAACCAA
 GTACCAAGTGAAGACTTTGAACGCACCTCCTCAGAGTCCGACTCTCCCACCTGCTAAGTCAAGTACCCCTACAA
 GACTGATGGAATTACAGTTGTAT**TAA**AATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT
 AGGCCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAAGGCACAGAGATTAGACGAGCTGTAAAGAACAC
 ATCTACTTTATGCAATGGCATTAGACATGTAAAGTCAGATGTCAATGTACAGTACGAGCCAAATCTTTGT
 TAAAAACCCCTATGTATAGTGACACTGTAGTTAAAGATGTTTTATTATATTTCAATAACTACCCTAACAA
 ATTTTTAACTTTTCATATGCATATTCGTATATGTGGTCTTTTAGGAAAAGTATGGTTAAATAGTTGATTTTCAA
 AGGAAATTTTAAATTTCTTACGTTCTGTTTAAATGTTTTTGTATTTAGTTAAATACATTGAAGGGAATACCCG
 TGCTTTTCCCTCTTTATGCACACAAACAGAAACGCGTTGTCATGCTCAAACTATTTTATTGTCACACTACA
 TGAATTCACCAATCTCTTAAACACGACATATAATAGATTTCCTGTATATAATAACTATACATACGCTCCA
 TAAAGTAAATCTTCAAGCTGTCTAGAACAAATCCTCCACTTCTCAGTGTCTCCGATTCGAACAGAGTTGATG
 ACAATATATAAATACTCAGTCCATATATAAAACTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACATA
 TATCAATATCTAAGTGATATATTTTTTAAGAAAGATTATTTCTCAATAACTTTCTAATAAATTAAGTTTAGTG
 TTTGGCCGCTCAACTCTCACTACTATTAGTAAGAACTTTAACTTTTAATGTGTAGTAAGGTTTATTTCTACCTT
 TTTCTCAACATGACACCAACACAACTCAAAACGAAGTACTGAGGTGCTAACTGTAGGATTAATCCAGTAT
 TCCGCTCACAATGCAATCCAGGAGGAGCTACCCATGTCACTGGAATTCGGCGATATGSGTTTATTTTTCTCTCC
 TGATTTGGATAACCAAATGGAAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTCTCGGCTT
 TTTTCTGGSCAAAGGGTGCCACTATTGGAGAGGTGGAAATATAAGTCTGAATCTGTAGGGAAGAGAACAT
 TAAGTATATTCAGAGGAAAAATCATCATCTATGTTCCAGATTCTCATTAAGACAAAGTTACCCACAACACT
 GAGATCAACTTAAGTGACATCTCTATTGTCAAGTCTAAATACATTAACAACTCATGTGTAATAGGCGTATAA
 TGTATAACGGTGACCAATGTTTCTGAATGCATAAAGAAATGAATAAATCAACACAGTACTCTCTAAACAA
 CTTCACCAAAAAAAGACCAAAACATGGAACGAATGGAAGCTTTGAAGGACATGCTTGTATTAGTCCAGTGGTTT
 CCACAGCTGGCTAAGCCAGGAGTCACCTGGAGGCTTTAAATACAAACATTTGAGCTGGAGGCCATTATCCTT
 AGCAAGCTAATGCAGAAACAGAAATCAACTACCGCATGTTCTCACTATAAGTGGGAGGTAAATGATAAGAACT
 TATGAACACAAAGAGGAAACATAGACATTGGAGTCTATTTGAGAGGGGAGGTTGGGAGAGGAAAGGAGGCA
 GAAAGATAACTATTGAGTACTGCCTTCAACCTGGGTGATGAATAATATGTACAACAAATCCCTGTGACACA
 TGTTTACCTATGGAACAAACCTTCATGTGATCCCTAAACCTAAATATAAGGTTAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA
 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTLQLSDIGTYQCKVKK
APGVANKKIHLLVVLVKPSGARCIVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTCCACCCACAGCTATGCCTCTGATTGGTGA
ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC
CAATTAAACACCAAGAAGAAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACT
AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTTCTGCCCTC
CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTGTGTCTCCCTTGCTGGGTTTTACCTGT
CTTCTCTGGAGCCAGGTATCAGGGGGCCAGGGCCAAGAATTCACATTTGGGCCCTGCCAAGT
GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT
GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTCAAAAA
CCACCACAATAGAACAGTCTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACACT
TGTGTTCTCATCTGAGTGTCAACATGCCACCCAGTCACAGAAATGAGATGTTTCCCATCAGAGAC
AGTGCTCACAGGGCGGTTTCTGCTATTCCGGAGAGACGATTCAAACAGTTGGACGTAGAGCAGC
TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC
TCTTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTCA
AACAGTCTCCCTTCCCTATGCTGTTCACTGGACACTTCACGCCCTTGCCATGGGTCCCATT
TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTGTATTATTACAACCTCTATTT
AATTAATGTCAGTATTTCAACTGAAGTTCATTATTATTGTGAGACTGAAGTTACATGAAG
CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTACAATCCTTGCCACAGTGTGGGGCAG
TGGATGGGTGCTTAGTAAGTACTTAATAAAGTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
GTTAAAAAACAGAGAGGGATGCTTGATGTAAACTGAACTTCAGAGCATGAAAATCACACT
GTCCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAAGTGCATCTGTTTGAAAG
TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTCATT
TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT
TATCTAGTCTACTTCTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
ATTCTGACCTGGATGTACTATCCAATCTGTGATGACATTCCTTGCTAATAAAGACAACATAA
CTCCAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPCPPLLATASQMOMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATGA**AGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGCTTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTTGACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVITILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCCEQ
RQCHCRQEATNATRVIHNDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGGCTACAATTAATACATAACCTTATGTATCATACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTTGCCCTTCTCTCCACAGGTGTCCACTCCAGGTCCAACCTGCACCTC
GGTTCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACGATGTTGGGGGGCCGCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGAC
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCCGGCCTCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY
DVIYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHNTPIPRRHTRS AEDDSE
RDPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCTTTCTTCTTCTGCTGGGAGGTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACC CGCAGAGCAGACACTGCATGACAACGGACGACACAGAAG
 TCCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGCCCATTC CAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTT CACAAAAACATCTCCCACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCGTACAGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCC
 GTCAGGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCGTCAT
 GGTCCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCTGGTGACTGTCACAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTC CAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCACTCTGC
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACC CGGGGCCACGACCCCTCAGTGGAGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGCTCTCCATAGAGGCTGGGT CAGCAGTGGGCAAAACAATTC
 CTTTGCTGGGAGCTCTGCTTCTCTCTACAGCCCTCGGAAGCGCCCTCAAGAACCTTACCCC
 CTT CAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCTT
 CTTCTTCTGTCTCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACCT**GA**GTGCAGGTGAAAATGGAGGTTTCTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGAAGACCTCACTGACCC CAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAACCTCACGCCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGT CAGGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGTGCTGCCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGTGTGAGAGGTACCCAGAGGTTC CCAATG
 AAGGCGAGCATGTCCAAGCCCTTAACCC CAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGGAGGGGCTTCACTGTTC CAGAGGTGTCCTTGGACTCACCTTGG
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCCATCTGTGTGCTTCCATCCTGCA
 TTAATAATCACTCAGTGTGGCCCAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQITIGSDPEEAFDITLCTDDSSSEAKLTMDILTLAHTSTEAKGLSSESSASSDGP
 HVPITPSRASESSASSDGP
 HVPITPSRASESSASSDGP
 HVPITPSWSPGSDVTLLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALS
 VETPSYVKVSGAAPV
 SIEAGSAVGKTSFAGSSASSYSPSEAAALKNFTPSETPTMDIATKGPFP
 TSRDPLPSVPPTTTNSSRGNTSLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGCGGATTGCGCCGCTCCTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGCGAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAAACTAAACTGAAATTTAAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTCTTGTCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCCGAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTCAAAATTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGCTACTTCTC
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTTCAAGCAGCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGGTGCTGTTCTCGGTGATAGGCC
 TCGTCTCTCGGGTAGAATCCTTTCCGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTCTGTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTTGGCCAGGCTGGAGTGCAGTAGCAGGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GCTCTCAAACCTCCTGACCTAGTGATCCACCCCTCCTCGGCCCTCCAAAGTGCTGGGATACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTGAAGAAGAAATGAAGTG
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTCACATCTTGGTTCAGATAAAATCAAC
 TGTTTTATCAATTTCTAATGGATTGCTTTTCTTTTATATGATTCCTTTAAACTTATT
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYDKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHLLPENV SALPATVAVASPHTT SATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWL LIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCACGGTGTCAGCGCCAGAA**ATG**CGGCTTCTGGTCTGCTATGGGGTTGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATTCTATGCAGAAGAAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAACGGGGCCCCGATGAG
 TCTTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACACGCCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCATTGGCCAGGGACTTCCCAGTACGGGCACGAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGCAGGGGAGCTCCCGCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTCTGAGCCTTCTGTTCAGC
 CGCAGGCCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGGAGAAAGGAACTCAACAGGCCA
 CGGAGCACAGAGGAAACGAGAAGTTCTGGCTCTCAGCGTTGACTCGGGGAGGAAAGGAAGCC
 CCTTCCAGGCCCCTGAGGGGGACGTGATCTCGATGCCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCG**TAG**GGCAGGAGGCCCTCCTGGCCAGGCCACGAGT
 GAAGCAGTAGTCTGGCTGGCTGAGTACGACACCGATTCCGAAAGGCTTGGCAGCTCAGCCCTCAGAT
 TCCAGTGTCCCGGAGTCCAGGGCTCTCCCCACCTCCCGAGGCTCTCCTCTGGATGTTTCA
 CGCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCGAGCGGTGGCCTTGTCTCTCCGCGTG
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGG
 CTCTATGCCCAGTGTGCGACCCTGCCCTTCCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTTGATTCCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCTAAACAATGCCAGTGAAGTGTGCGACTTGAAGTTTGAAGGCCAGTGGGCCCT
 ATGAACGCTCACACCCCTTCAAGCTTAGAGTCTGCATTGGGCTGTGACGCTTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCTCTTNCATTTGGCTCCCTGGNCCATGCTTCTTGGCTTTGGGAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAAACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCGAGAGGGGCTCGGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTTCTTTTTCCATTATTTGTTTTTAAAGACAGAAATCTCGTGCT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCTCTCGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCTCCTGTCTTCACTTCCCAAATGCGGGGATACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTCACCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTGACTTCTTCCCTCTTTCTCTCTTCCATTAATTTGCCGGTGTCTT
 TTTACAGAGCAATATCTTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCAGCTCTCTGTGTTTTACAGACCTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDQAGEYWCCVEKRGPDDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
TSQYGHERTSQYTGTSPHPATSPPPAGSSRPPMLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLLVLLSLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128